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AJ245935
AJ245935.1 GI:7018604
Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne,
                                                                                                             Ibberson,M., Uldry,M. and Thorens,B. GLUTXI, a novel mammalian glucose transporter central nervous system and insulin-sensitive ty. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                 glucose transporter;
Norway rat
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Pred. No. 1.9e-146;
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Sciurognathi; Muridae; Murinae;
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                              20283667
2 (bases 1 to 1490)
Joost, H.G.
                                                         Doege, H., Schurmann, A., Bahrenberg, G., Brauers, A. and Joost, H.G. GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawachi, Tochigi 329–0498, Japan (E-mail:kishiba@jichi.ac.jp,
Tel:81-285-58-7326, Fax:81-285-44-5541}
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1490)
                                                                                                                                                                                        Mus musculus
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IMFYANTIFEEAKFKDSSLASVIVGIIQVLETAVAALLMDRAGRKLLLALSGVIMVFS
MSAFGIYFKLTGOSFOSNSSHVGLLVPISADEPADVHLGLAWLAVGSMCLFIAGFAVGWG
PIPWLLMSEIFPLHIKGVATGVCVLTTNWFMAFLVTKEFNSIMEILRPYGAFWLTAAFC
ILSVLETLTSVPETKGRTLEQITAHFEGR"

3 702 c 609 g 486 t
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LCTVPFVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGS
CVQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHQYQE
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/protein_id="BAA94383.1"
/db_xref="gi:7592444"
/translation="MSPEDPQETQPLLRSPGARAPGGRRVFLATFAAALGPLSFGFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="glut8"
109. .1548
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                            GI:7688219
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                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1843)
Carayannopoulos,M.O., Chi,M.M., Cui,Y., Pingsterhaus,J.M.,
McKnight,R.A., Mueckler,M., Devaskar,S.U. and Moley,K.H.
                                                                                                                                                                                                                   Submitted (07-FEB-2000) OB/Gyn, Washington University, 4566 Scott Ave, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                             Moley, K.H., Carayannopoulos, M.O. Direct Submission
                                                                                                                                                                                                                                                                                                                                         glucose uptake in the blastocyst Proc. Natl. Acad. Sci. U.S.A. 97
                                                                                                                                                                                                                                                                                                                                                                              GLUT8 is a glucose transporter responsible for insulin-stimulated
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
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/codon_start=1
/product="glucose transporter GLUT8"
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/db_xref="GI:8671758"
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VQLMVVTGIILLAYVAGWVLEWRWLAVLGCVPPTLMLJLMCYMPETPRFLLTQHQYQEA
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GYSSPAIPSLRRTAPPALRLGDNAASWFGAVVTLGAAAGGILGGWLLDRAGRKLSLLL
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/protein_id="CAB89815.1"
/db_xref="gI:7688220"
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                                                                                                                                       /strain="129"
                                                                                                                                                            /organism="Mus musculus'
                                                                                                                                                                                Location/Qualifiers
1. .1843
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/db_xref="taxon:10090"
                                                                                                                   /db_xref="taxon:10090"
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8.7e-17;
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                                                                               Mus sp.
                                                                                                                                                   l Similarity 100.0%; 50; Conservative 0;
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50; Conser
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AX076671
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1 (bases 1 to 2072)
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GYSSPALPSLRRTPPALLLGNAASWFGAVVTLGAAAGGILGWLLDRSGRKLSLLL
CTVPFVTGFAVTTAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYYPAVRGLLSGV
VQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHQYQEA
MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
                                                                                                                                                                                                                                                                                                        MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                                                                          VQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLLMCYMPETPRFLLTQHQYQEA
MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
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PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
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673 c 584 g 464 t
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21. .1454
                                                                                                                                                                                                                                                                                            PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL
                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAC28497.1"
/db_xref="GI:12711203"
/translation="MSPEDPQETQPLLRPPEARTPRGRRVFLASFAAALGPLNFGFAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus sp."
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8.6e-17;
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                                                                                                                                                                                                                                                                                                                                                               Bos taurus
Eukaryota;
                                                               1 (bases 1 to 1012)
Augustin,R., Navarrete-Santos,A. and Fischer,B.
Direct Submission
                                                                                                                                                                                                                          Bos taurus glucose transporter 8
AF321324
AF321324.1 GI:14582715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues
                              Submitted (13-NOV-2000) Anatomy and Cell Biology, Faculty of Medicine, Martin Luther University Halle, Grosse Steinstrasse
                                                                                                                      Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                             AF321324
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J. Biol. Chem. 275 (7), 4607-4612 (2000)
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                  Halle
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                  061097,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glucose transporter"
/protein_id="CAB75719.1"
/protein_id="CAB75719.1"
/db_xref="G1:7018607"
/db_xref="G1:7018607"
/translation="MSPEDPOETOPLLRPPEARTPRGRRVFLASFAAALGPLNFGFAL
/translation="MSPEDPOETOPLLRPPEARTPRGRRVFLASFAAALGPLNFGFAL
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CTVPFVTGFAVTTAARDVMMLLGGRLLTGLAGGVASTVAPVY ISETAVPAVRGILGSC
VQLMVVTGILLAYVAGWLENRWIAVLGCVPFTLMLLLMCTVPETPRFLTTOHOYOEA
MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGITXPLIIGISLMVFQQLSGVNAI
MFYANSIFEEAKFKDSSLASVTVGIIQVETTAVAALLMDRAGRRLLAALSGVLMVFSM
MFYANSIFEEAKFKDSSLASVTVGIIQVETTAVAALLMDRAGRRLLAALSGVLMVFSM
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                                                                                                                                 ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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100.0%;
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Sciurognathi;
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8.5e-17;
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                                                                                                                                      Pecora; Bovoidea
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J. Biol. Chem. 275 (21), 16275-16280 (2000)
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27. .1460
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                                 GYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLL
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/db_xref="G1:7688146"
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EAADTNVGLAWLAVGNMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGVCVLTNWF
MAFLVTKEFSSLMEVLRPYGAFWLASAFCIFGVLFTLACVPETKGKTLEQITAHFEGR
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH-1005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ibberson, M.R.
Direct Submission
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SVLFTFSCVPETKKKTLEQITAHFEGR*
3 519 c 477 g 318 t
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4. .1437
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 0104145-A 1 18-JAN-2001;
University of Lausanne (CH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 2080)
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320
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                                                                                                   /protein_id="CAC28495.1"
/db_xref="GI:12711199"
/db_xref="GI:12711199"
/translation="MTDEDPETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFAL
GYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLL
GYSSPAIPSLQRAAPADVMMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSC
VQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA
MAALRFLWGSEDGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAPQQLSGVNAVM
SVLFTLFCVPEIKGKTLEQITAHFEGR"
1 750 c 672 g 475 t
                                                            FYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTS
AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGNMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                                         348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="toxon:9606"
/note="Incyte ID No: 1416107CB1"
/note="Incyte ID No: 460 t
                                          PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
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                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No.
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WO0146258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids encoding same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen, D.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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COMMENT
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Best Local
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  misc_teature
                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity nes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATCCCCTGGCTCCTCATGTCAGAGATCTTCCCTCTGCA 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 26, 2001 this sequence version replaced gi:13277497.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of clone RP11-356B19 The true left end of clone RP11-373J8 is at 96439 in this sequence. The tright end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RP11-356HJ9 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laird, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3
                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 225370)
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  /note-"Single clone region. Sequence from reads from short insert library derived from a single pUC clone. Restriction digest data confirm the assembly." 225123. . . 225370
                                                                                                                                                                 /clone="RP11-356B19"
/clone_lib="RPCI-11.2"
23455. .23821
                                                                                                                 /note="Single clone region. Assembly confirmed by
restriction digest data."
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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Pred. No. 9.1e-12;
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  REFERENCE
                                                                                                                   SOURCE
                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                       CGRHOD
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ORIGIN
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                                                                                                                                         KEYWORDS
                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                  RESULT
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Cricetulus
1 (bases )
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AX191507
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  (bases 1 to 11931)
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881 GGCAGCATGTGCCTCTTCATCGC 903
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Cricetulus griseus
Eukaryota; Metazoa; Chordata;
Mamumalia; Eutheria; Rodentia;
                                                                                                             CGRHOD 11931 bp
C.griseus rhodopsin
X61084
                                                         opsin; rhodopsin; vision protein Chinese hamster.
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1 (bases 1 to 1461)
Kato,S. and Kimura,T.
                                                                                           X61084.1 GI:49478
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Direct Submission
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Localization and DNA sequence of a replication origin in the rhodopsin gene locus of Chinese hamster cells
J. Mol. Biol. 224 (2), 343-358 (1992)
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insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB66934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-2000;
13-JUL-2000;
(GEMY ) GENETICS
                               15-OCT-1998;
                                                              15-OCT-1999;
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2072 BP; 351 A; 673 C; 584 G; 464 T;
                                                                                           20-APR-2000
                                                                                                                                                                                     tumour; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                          immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .g. ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-112615/12.
                                                                                                                                                                                                                                                                                                                                                                          mouse; chicken; rat; secreted expressed sequence tag;
sed sequence tag; EST; probe; chemotactic; proliferati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 73-74; 124pp; English.
                                                                                                                                                                                                                                                                                                                            antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ibberson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0184285
2000US-0616132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \ensuremath{\mathsf{n}}, diagnosis and treatment of hexose transport disorders, and diabetes -
                               98US-0104436
                                                            99WO-US24206
INST
                                                                                                                                                                                     depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                     psoriasis;
                                                                                                                                                                                                                                                                                                                                                                          chemotactic; proliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
5.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                         SEST;
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molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzhelmer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemotactic; proliferative; immunomodulatory; haematopoietic;
chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 586; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anticonvulsant; and antidepressant. The sESTs can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the tissues they were isolated from. The activities include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue sources. The sESTs can have a range of activities depending
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to AAA45925 represent specifically claimed tags (sESTs), isolated from human, mouse, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparkinsonian; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCoy JM,
Treacy M,
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Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs and genomic DNA ne sESTs. Proteins encoded by the sESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse, chicken and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted expressed
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AAD09552
ID AADC
AAD09552
                                               AAD09552 standard; cDNA;
                                               2080
                                               ВP
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Human transporter and ion channel-1 (TRICH-1) cDNA

10-SEP-2001

(first entry)

DЬ 20

Matches Query Match Best Local :

Similarity 100. 41; Conservative

100.0%; 14.5%;

Score 41; Pred. No.

DB 21; . 2.1e-11

Length 579, Indels

0

Mismatches

0

0;

Gaps

0;

Sequence

579

BP; 109 A; 184 C;

180 G;

106 T; 0 other;

demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocardits; Grave's disease dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stro gene therapy; amyotrophic lateral sclerosis; hypertension; angina; neurological disorder; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; Human; transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis; hypercholesterolaemia; asthma; bipolar disorder; amnesia; muscular dystrophy; Grave's disease; stroke;

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AAF55865
ID AAF!
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                                                                                                                                                                                                    RESULT
                                                                                                                                   Matches
                                                                                                                                                                                                                                    including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999;
14-JAN-2000;
21-JAN-2000;
28-JAN-2000;
02-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                              cystic for disease,
                                                                               1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is transporter and ion channel-1 (TRICH-1) cDNA TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                      disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating disease, mental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
             AAF55865 standard;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                             purposes
                                                                                                                                                                                                                                                                                                                                                                                                                              disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzhelmer's disease, amnesia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2000;
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                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing transport, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-418042/44.
                                                                                                                                              Similarity
                                                                                                                                                                                                    2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 140-141; 160pp; English.
                                                                                                                                14.5%; ilarity 100.0%; Conservative
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Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0177332.
2000US-0178572.
2000US-0179758.
2000US-0181625.
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2000US-0176083
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                                                                                                                                                                                                    вP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Human TRICH-1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                    300
             cdna;
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Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC
                                                                                                                                                                                                    889
               2217
                                                                                                                                   0
                                                                                                                                              Score 41;
Pred. No.
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             ВР
                                                                                                                                                                                                    632
                                                                                                                                 Mismatches
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Nguyen
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                                                                                                                                                                                                    460
                                                                                                                                            DB 22; I
2.2e-11;
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DB,
                                                                                                                                                                                                   T; 0 other;
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Yao MG,
                                                                                                                                 0
                                                                                                                                                          Length 2080;
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Gandhi
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                                                                                                                                                                                                                                                                                                                                                                                                                               bipolar
                                                                                                                              Gaps
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RESULT
AAD12574
Вb
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                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                      cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
                                                                                                                                                                                                                                1518 cccatcccctggctcctcatgtcagagatcttccctctgca 1558
                                                             Human; hydrophobic
                                                                                       Human
                                                                                                                                          AAD12574;
                                                                                                                                                                 AAD12574
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disore, is chemia and diabetes -
                                                                                                                 25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2001
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                                                                                                                                                                                                                                              cccatcccctggctcctcatgtcagagatcttccctctgca
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DB; AAB66932.
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                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                   2217
                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 70-71; 124pp; English
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ibberson
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0184285
2000US-0616132
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                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                      having hydrophobic domain encoding cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0143907
99US-0151140
                                                                                                                                                                                                                                                                                                                                                   320 A; 750
                                                            domain; gene therapy; nutritional supplement;
                                                                                                                                                                    cDNA; 1461
                                                                                                                                                                                                                                                                                              14.5%;
100.0%;
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                                                                                                                                                                                                                                                                                   0,
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   672 G;
                                                autoimmune disorder; antimicrobial;
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                                                                                                                                                                                                                                                                                              DB 22;
2.2e-11
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                                                                                                                                                                                                                                                                                                          Length 2217;
                                                                                                                                                                                                                                                                                                                                                   other;
                                                                                                                                                                                                                                                                                     Indels
                                                                                       HP10784.
                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
                                                                                                                                                                                                                                                                                   Gaps
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disease; Alzheimer's disease;

thrombolytic;

tumour growth inhibitor;

anabolic;

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RESULT 7
AAI14336/C
ID AAI14336 standard;
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                                                                                                             B
                                                                                                                                                                                                             Query Match
Best Local
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06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                 supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate activin and inhibin activity, to modulate receptor modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is human protein with hydrophobic domain encoding CDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 287-289; 563pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROT-)
(SAGA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000; 2000WO-JP09359
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                                                                                                             881 ggcagcatgtgcctcttcatcgc
                                                                                                                                43 ggcagcatgtgcctcttcatcgc 65
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23; Conser
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                                                                                                                                                                                                                                                                                                 1461
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2000JP-0000588.
2000JP-0002299.
2000JP-0026862.
2000JP-0058367.
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                 ВP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Τ;
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/product= "Human protein having hydrophobic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "CDS is specifically is claimed in claim
                                                                                                                                                                                                                                                                                                 195
        DNA;
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          423
                                                                                                                                                                                                                                                                                              501 C;
        ВΡ
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Pred. No.
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IID AAI357
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Probe
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KW geneti
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Best Local
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26-MAY-2000; 3
30-JUN-2000; 3
03-AUG-2000; 2
21-SEP-2000; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                           genetic disorder;
                                                                                                                              17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing
                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                   Probe #4399 used to measure gene expression in human placenta sample.
                                                                                                                                                                       AAI35713;
                                                                                                                                                                                                             AAI35713 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 423
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analyzing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #4269 for gene expression analysis in human cervical cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 4269; 487pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
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e. The SENPs are derived
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probes

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RESULT 9
AA104170/c
1D AA104170 standard; D
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AC AA104170:
XT
DT 09-OCT-2001 (first.
XX
DE Probe #4161 used to |
XX
DE Probe; human; breast
KW Probe; human; breast
KW Inflammatory disease
XX
PN WC200157270-A2.
XX
PN WC200157270-A2.
XX
PP 29-JAN-2001; 2000US-PR 26-MAY-2000; 2000US-PR 30-JUN-2000; 2000US-PR 10-SEP-2000; 2000US-PR 21-SEP-2000; 
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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expression in samples derived from human placenta. The
for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACCTGGGGCTGGCCTGGC 157
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
   2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast disease; breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human breast sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SENP).
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RESULT 10
AAI23539/c
ID AAI235
XX AAI235
XX Probe;
XW Probe;
XW CCETVIC
XX Probe;
XW CCETVIC
XX Homo s
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                   30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a human breast sample, where hybridises at high stringency to a nucleic acid expressed in the breast. The probes are useful for predicting, diagnosing, grading staging, monitoring and prognosing diseases of the human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                        27-SEP-2000;
                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #13472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI23539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI23539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel single exon nucleic acid p The present sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel single exon nucleic acid in a human breast .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-carcinoma tumours
                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
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                                                                  sg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACCTGGGGCTGGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcacctggggctggcctggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 7.1%; Sil Similarity 100.0%; 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS
                                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-02346359.
                                                                                                                                                                                                                                                                                                                           2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N<sub>O</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ę
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                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                  DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            part of the printed
directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grading,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         where the probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes
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2001-488901/53

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AAI48856/c
ID AAI48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                     04 FEB-2000;
26 MAY-2000;
30 JUN-2000;
03-AUG-2000;
21 SEP-2000;
27 SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging
          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                             analyzing
                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                              Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #17542 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI48856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from human HeLa cells.
                                                                                                                                                                                (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 tcacctggggctggcctggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TCACCTGGGGCTGGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases of the cervix, notably cervical cancer.
                                                                                                                                  2001-488897/53
                                                                                                                                                         SG
                                                                                             genome-derived single exon nucleic acid zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                        Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                     2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234635
2000US-0236359
2000US-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                              2000US-0180312
                                                                                                                                                                                                                                                                                                    2001WO-US00663
                                                                       ID
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                                                                                                                                                        DK,
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                                                                      No 17542;
                                                                                                                                                                                                                                                                                                                                                                                                    ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     to measure
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                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
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                                                                                                                                                                                                                                                                                                                                                                                                              placenta;
                                                                   654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             βP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                        Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                     expression in human placenta
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                                                                                                                                                        DR
                                                                                                                                                                                                                                                                                                                                                                                                               antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Τ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                       probes useful
                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                     sample
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RESULT 1
AAI09165/
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                 04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                         measuring human gene expression in a human breast sample, where the pri
hybridises at high stringency to a nucleic acid expressed in the human
breast. The probes are useful for predicting, diagnosing, grading,
staging, monitoring and prognosing diseases of the human breast,
                                                                                                                                                                                       Novel
in a l
                              Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                           particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseas of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                   The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for
                                                                                                                                                                   Claim
                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 465 BP; 113 A; 137 C;
Sequence
                                                 non-carcinoma tumours
                                                                                                                                                                                                                     WPI; 2001-476286/51
                                                                                                                                                                                                                                                              (MOLE-)
                                                                                                                                                                                                                                                                                    04-OCT
                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                            WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #9156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI09165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT09165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                       single exon nucleic acid
human breast ·
                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
20; Conserv
                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 465
                                                                                                                                                                   SEQ ID No
                                                                                                                                                                                                                                         Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used
                                                                                                                                                                                                                                                                                            2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 BP;
                                                                                                                                                                                                                                                                                                                                                2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast
 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                   9156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
 Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative breast disease; non-carcinoma
 137
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                                                                                                                                                                 322pp;
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C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast
 136
                                                                                                                                                                                                  probe
                                                                                                                                                                                                                                           Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                   English
 G;
                                                                                                                                                                                                  used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
 79
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  Τ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0 other;
                                                                                                                                                                                                to measuring
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 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                               development disorder;
 other;
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                               part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast sample
                                                                                                                                                                                                  gene
                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                       diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour.
                                                                                                                          probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Query Match Best Local S Matches 20

Similarity 20; Conser

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

100.0%;

Score 20; Pred. No

NO.

DB

22;

Length 465;

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RESULT 14
AAV37386/c
ID AAV37386 standard; D:
XX
AC AAV37386;
XX
DT 13-OCT-1998 (first e
                                                                                                                                                                                                                                                                                                                        RESULT 13
AAX308
AX Strept
XX Strept
XX Strept
XX W9737
XX W97737
XX 01-APR
XX 02-AUG
PR 02-APR
XX 01-APR

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black MT, n
                                                                                                                                                                                                                                                                                                                                                                      AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0109933. These genomic DNA sequences encode the novel proteins given in AAY11114 to AAY11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
streptococcal
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                             protective immune response in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding pneumococcal polypeptide(s) - vaccines, drug screening, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1996;
02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1999
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                                                                                                                                                                692
                                                                                                                                                                                 255 cttctgtatcctcagcgtc 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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DB; AAY11256.
                                                                                                                                                                                                                                   l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                          954 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 128; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hodgson JE,
                                                                                                                                                                                                                                   Conservative
 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae strain 0100993; vaccine;
infection; pneumococcal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae genomic DNA sequence SEQ ID NO:116.
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96US-0014690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US05306
                                                                                                                                                                                                                                                                                                                          279 A; 171 C;
                                                                        DNA;
                                                                                                                                                                                                                           6.7%; 5c.
100.0%; Pr
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                                                                         2051 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                     Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                          278 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholas
                                                                                                                                                                                                                                                   DB 18;
3.6;
                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                      954;
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                                                                                                                                                                                                                               Gaps
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                                                                                                                                            Вb
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RESULT 15
AAH57375/c
ID AAH57375 standard;
                                                                                                                                                                                                                                                                                                               S. pneumoniae. Its encoded protein, or agonists of it,

may be useful as an antibacterial for treatment or

prevention of infection, specifically caused by S. pneumoniae

(particularly meningitis) but possibly also Helicobacter

pylori (ulcers and gastric cancer). It may be of particular

use before insertion of an in-dwelling device or any other

invasive procedure. The protein, or nucleic acid encoding

it, can also be used in vaccines to induce a cellular

and/or humoral immune response, or to screen for other

antibacterials. The DNA may also contain flanking sequences

that are potential sources of control elements for bacterial

gene expression. Detecting a sequence encoding the protein

can be used diagnostically, e.g. to detect a mutation for
                                                                                                                                                                      Matches
                                                                                                                                                                                                         Query Match
                                                                                              1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of a coding region isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                    serotyping or classifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acids from Streptococcus pneumoniae e.g. for identifying anti-bacterial(s) for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding region; ORF; open reading frame; antibacterial;
infection; prevention; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                255 cttctgtatcctcagcgtc 273
                                                                                                                                                                                       Local
                                                                                              CTTCTGTATCCTCAGCGTC
                                                                                                                                                                      Similarity
19; Conserv
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                                                                                                                                                                                                                                                               2051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hodgson J
Zarfos PN;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91-92; 130pp; English.
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979..1932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                               569 A; 358 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW60997
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   CDNA;
                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                         6.7%;
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                                                                                              1591
   4214
                                                                                                                                                                                                                                                                                                  infectious agents.
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                                                                                                                                                                      0;
                                                                                                                                                                                         Score 19;
Pred. No.
 ΒP
                                                                                                                                                                                                                                                               458 G;
                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                       3.6;
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                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                      0;
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                                                                                                                                                                                                         Length 2051;
                                                                                                                                                                      Indels
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    useful,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention
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10-SEP-2001

(first entry)

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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                        mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of [1] in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a concerning control of the same control of the same control of the same can be used for diagnosis.
                                                                                                  2147 CTGGGGCTGGCCTGG 2129
                                                                                                                                                                                                                                                                                   Sequence 4214 BP; 930 A; 1213 C; 1343 G; 727 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences (1). (1) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (1) and proteins (11) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 145-146; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
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972 13 4.6 3117 1 973 13 4.6 3125 1 974 13 4.6 3236 4 975 13 4.6 3238 4 976 13 4.6 3238 4	969 13 4.6 3103 3 970 13 4.6 3103 4 971 13 4.6 3111 3	967 13 4.6 3103 3 968 13 4.6 3103 3	964 13 4.6 3040 4 965 13 4.6 3059 1 966 13 4.6 3097 4	963 13 4.6 3040 4	961 13 4.6 3006 4 962 13 4.6 3024 1	959 13 4.6 2943 1 960 13 4.6 2952 1	13 4.6 2931 3	13 4.6 2928 5 13 4.6 2928 5	13 4.6 2928 2	13 4.6 2928 2 13 4.6 2928 2	13 4.6 2928 2	13 4.6 2928 2 13 4.6 2928 2	13 4.6 2928 2	13 4.6 2928 2	13 4.6 2906 1	945 13 4.6 2880 2	943 13 4.6 2848 4	13 4.6 2823 2	13 4.6 2815 3	13 4.6 2812 2	13 4.6 2812 1 13 4.6 2812 1	13 4.6 2812 1	934 13 4.6 2808 3	933 13 4.6 2799 2	13 4.6 2728 3	930 13 4.6 2710 4	929 13 4.6 2710 4	92/ 13 4.6 2710 4 928 13 4.6 2710 4	926 13 4.6 2709 4	925 13 4.6 2693 4	924 13 4.6 2693 4	13 4.6 2688 2	13 4.6 2688 1	13 4.6 2688 1	918 13 4.6 2677 4 616 13 4.6 2688 1	917 13 4.6 2672 3	915 13 4.6 2669 4 916 13 4.6 2669 4	914 13 4.6 2663 3	913 13 4.6 2663 2	912 13 4.6 2663 1	911 13 4.6 2661 1	909 13 4.6 2630 3	908 13 4.6 2630 3	907 13 4.6 2630 2	906 13 4.6 2612 4	904 13 4.6 2609 4
972 13 4.6 3117 973 13 4.6 3125 974 13 4.6 3236 975 13 4.6 3238 976 13 4.6 3238	969 13 4.6 3103 3 970 13 4.6 3103 4 971 13 4.6 3111 3	967 13 4.6 3103 3 968 13 4.6 3103 3	964 13 4.6 3040 4 965 13 4.6 3059 1 966 13 4.6 3097 4	963 13 4.6 3040 4	961 13 4.6 3006 4 962 13 4.6 3024 1	959 13 4.6 2943 1 960 13 4.6 2952 1	13 4.6 2931 3	13 4.6 2928 5 13 4.6 2928 5	13 4.6 2928 2	13 4.6 2928 2 13 4.6 2928 2	13 4.6 2928 2	13 4.6 2928 2 13 4.6 2928 2	13 4.6 2928 2	13 4.6 2928 2	13 4.6 2906 1	945 13 4.6 2880 2	943 13 4.6 2848 4	13 4.6 2823 2	13 4.6 2815 3	13 4.6 2812 2	13 4.6 2812 1 13 4.6 2812 1	13 4.6 2812 1	934 13 4.6 2808 3	933 13 4.6 2799 2	13 4.6 2728 3	930 13 4.6 2710 4	929 13 4.6 2710 4	92/ 13 4.6 2710 4 928 13 4.6 2710 4	926 13 4.6 2709 4	925 13 4.6 2693 4	924 13 4.6 2693 4	13 4.6 2688 2	13 4.6 2688 1	13 4.6 2688 1	918 13 4.6 2677 4 616 13 4.6 2688 1	917 13 4.6 2672 3	915 13 4.6 2669 4 916 13 4.6 2669 4	914 13 4.6 2663 3	913 13 4.6 2663 2	912 13 4.6 2663 1	911 13 4.6 2661 1	909 13 4.6 2630 3	908 13 4.6 2630 3	907 13 4.6 2630 2	906 13 4.6 2612 4	904 13 4.6 2609 4
972 13 4.6 3117 1 US-08-172-331B-3 Sequenc 973 13 4.6 3125 1 US-08-162-809-19 Sequenc 974 13 4.6 3236 4 US-08-927-219-7 Sequenc 975 13 4.6 3238 4 US-08-927-219-3 Sequenc 976 13 4.6 3238 4 US-08-927-219-3 Sequenc	969 13 4.6 3103 3 US-09-126-640-2 Sequence 2 970 13 4.6 3103 4 US-08-925-88-3 Sequence 3 971 13 4.6 3111 3 US-09-487-444-3 Sequence 3	967 13 4.6 3103 3 US-08-826-246-3 Sequence 3 968 13 4.6 3103 3 US-08-944-495-3 Sequence 3	965 13 4.6 3059 1 US-09-282-147-38 Sequence 38 965 13 4.6 3059 1 US-09-282-147-38 Sequence 38	963 13 4.6 3040 4 US-09-378-255-3 Sequence	961 13 4.6 3006 4 US-09-552-351-1 Sequence 1, 962 13 4.6 3024 1 US-07-923-976-7 Sequence 7.	959 13 4.6 2943 1 960 13 4.6 2952 1	13 4.6 2931 3 US-08-943-956A-1 Sequence	13 4.6 2928 5 PCT-US95-02058-1 Sequenc	13 4.6 2928 2 US-08-479-895-1	13 4.6 2928 2 US-08-487-797-3 Sequenc	13 4.6 2928 2 US-08-487-797-1 Sequence	13 4.6 2928 2 13 4.6 2928 2	13 4.6 2928 2 US-08-436-771-3 Sequenc	13 4.6 2928 2 US-08-436-771-1 S	13 4.6 2906 1 US-08-554-612C-49 Sequenc	945 13 4.6 2880 2 US-08-500-857A-3 Sequence 3	943 13 4.6 2848 4 US-08-464-954A-2 Sequence 2	13 4.6 2823 2 US-08-893-333-1 Sequenc	13 4.6 2815 3 US-09-214-564A-1 Sequence 1	13 4.6 2812 2 US-08-920-828-16 Sequence 1	13 4.6 2812 1 US-08-921-177-16 Sequence 1	13 4.6 2812 1 US-08-920-827-16 Sequence 1	934 13 4.6 2808 3 US-08-870-126-7 Sequence 7,	933 13 4.6 2799 2 US-08-874-186-42 Sequence 4	13 4.6 2728 3	930 13 4.6 2710 4 US-09-232-197-70 Sequence 70	929 13 4.6 2710 4 US-09-232-197-44 Sequence	928 13 4.6 2710 4 US-09-232-200-70 Sequence 7	926 13 4.6 2709 4 US-09-251-372-1 Sequence 1	925 13 4.6 2693 4 US-09-561-138-5 S	924 13 4.6 2693 4 US-09-141-212-5 Sequence	13 4.6 2688 2	13 4.6 2688 1 US-08-441-750-3 Sequence	13 4.6 2688 1	918 13 4.6 2677 4 US-08-882-164D-36 Sequence	917 13 4.6 2672 3 US-09-214-564A-5 Sequence 5	915 13 4.6 2669 4 916 13 4.6 2669 4	914 13 4.6 2663 3 US-09-275-925-4 Sequence	913 13 4.6 2663 2 US-09-073-594-4 Sequence 4	912 13 4.6 2663 1 US-08-653-740-4 Sequence 4	910 13 4.6 2650 4 05-09-031-626-1 5	909 13 4.6 2630 3 US-09-032-894-1 S	908 13 4.6 2630 3 US-08-890-979-1 Sequenc	907 13 4.6 2630 2 US-08-890-980-1 Sequence	906	904 13 4.6 2609 4 US-09-141-212-7 S

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; MOLECULE TYPE: US-08-808-982-3
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US-08-808-982-3
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GENERAL INFORMATION:
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                                                                                                                          TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Masu, Masayuki
APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: NUTTI Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                        REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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ZID.

"LUNESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZID.

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                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                    2831 base pairs
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Masu, Masayuki
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US-08-261-206A-71
US-08-486-270-1
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US-08-367-264-1
US-08-08-252-574C-10
US-08-08-097-997A-10
US-08-946-994-1
US-08-946-994-1
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US-07-913-593-1
US-07-913-593-1
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US-08-321-670-1

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US-09-225-170-11
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RESULT 3
US-08-036-555B-44/c
; Sequence 44, Application US/08036555B
; Patent No. 5530109
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US-09-306-902A-3
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Best Local S
Matches 18
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GENERAL INFORMATION:
            GENERAL INFORMATION:
APPLICANT: Goodea
APPLICANT: Minghe
                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
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 APPLICANT:
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                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tessier-Lavigne, Marid
                                                                                                                                                                              CTGGGGCTGGCCTGGCTG 1486
                                                                                                                                                                                                                                                     18;
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2831 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 343-4341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/306,902A
Goodearl, Andrew; Stroobant, Paul;
Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
Chen, Maio Su; Hiles, Ian
                                                                                                                                                                                                                                                      Conservative
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Hink, Lindsay
Masu, Masayuki
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100.0%; Pred. No. 3.
tive 0; Mismatches
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US-08-469-569-44/c
; Sequence 44, Application US/08469569
; Patent No. 5606032
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
PHILING DATE: 30-JUN-1992
                                                 APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa: Waterfield, Michael; Marchioni,
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/965,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Glial Mitogenic Factors, Their TITLE OF INVENTION: Preparation and Use NUMBER OF SEQUENCES: 184
                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                  103 TGGTTTTGCAGTAGGC 88
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                                                                                                                                                                                                                                                                                                     66 tggttttgcagtaggc 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: singl
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FILING DATE: 03-APRIL-1992
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805 Third Avenue
2: Felfe & Lynch
805 Third Avenue
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US-08-249-322A-44/c
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                                                                                                                                                                                                                         Sequence 44, Application US/08249322A Patent No. 5716930
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                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                        APPLICANT: Goodearl, Andrew; Stroobant, Paul; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, APPLICANT: Chen, Maio Su; Hiles, Ian
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APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
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CURRENT APPLICATION DATA:
                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                            NUMBER OF SEQUENCES:
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COUNTRY: USA
ZIP: 10022
                              STATE: New York
                                           STREET: 805 Third Avenue CITY: New York City
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                                                                                                                          Preparation and Use
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                                                                                                            184
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Patent No. 5
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Best Local Similarity
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APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
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FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/96
FILING DATE: 23-0CT-1992
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PRIOR APPLICATION DATA:
08/036,555
                                                                      CORRESPONDENCE ADDRESS
                                                                                   TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 187
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
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TOPOLOGY: li
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COUNTRY: USA
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Minghetti, Luisa
Waterfield, Michael
Marchionni, Mark
Chen, Maio Su
                                         E: Clark & Elbing LLP
176 Federal Street
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32;
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Best Local
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                                           COUNTRY: U.S.A. ZIP: 02110
                                                                                  STREET: 176 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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COMPUTER:
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Sequence 44, Application US/08734591A Patent No. 5854220
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INFORMATION FOR SEQ ID NO
                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                             TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 TGGTTTTGCAGTAGGC 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/863 FILING DATE: 03-APRIL-1992
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FILING DATE: 03-SEP-1992
                                                                                        Massachusetts
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                                                                                                                          176 Federal Street
                                                                                                                                                                                                                                  Marchionni, Mark
Chen, Mario
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                                                                                                                                                                                                                                                                                         Minghetti, Luisa
Waterfield, Michael
                                                                                                                                                                                                                                                                                                                                              Goodearl, Andrew
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IBM Compatible Pentium
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100.0%; Pred. No.
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Gaps

CURRENT APPLICATION DATA:

OPERATING SYSTEM: Windows95 SOFTWARE: WordPerfect (Vers

WordPerfect (Version 7.0)

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Best Local Similarity 100.0%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                    Sequence 181, Application US/08469660 Patent No. 5876973
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                             APPLICANT: Gwynne, David I.; Marchionni, Mark; APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION, THEIR PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEPAX: (617) 428-7045
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                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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PRIOR APPLICATION NIMBER: 07/940,389
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PRIOR APPLICATION NUMBER: 08/036,555
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                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                            STATE: Massacn
ZIP: 0211-2804
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                                                                                                                 STREET:
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               COMPUTER:
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                               Diskette, 5.25 inch, 360 kb storage
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ER: 04585/00200P
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; NAME/KEY: CDS
; LOCATION: (1)...(569)
US-08-341-018-43
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                                                                                                                                                                                      CURRENT APPLICATION NUMBER: U5/08/341,018A
CURRENT FILING DATE: 1994-11-17
NUMBER OF SEO ID NOS: 87
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 43
LENGTH: 569
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08341018A Patent No. 6087323
Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     APPLICANT: Bermingham-McDonogh, Olivia
APPLICANT: Goldin, Stanley M.
APPLICANT: McBurney, Robert M.
APPLICANT: McBurney, Robert M.
TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS
TITLE OF INVENTION: CELLULAR COMMUNICATION
FILE REFERENCE: 04585/041001
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mahanthappa, Nagesh K. APPLICANT: Marchionni, Mark A.
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PRIOR APPLICATION NUMBER: 07/984
APPLICATION NUMBER: 07/984
APPLICATE: 01-DEC-1992
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                                                                                                                                                                     ORGANISM: Homo sapiens
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LENGTH: 569
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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5.7%; Score 16; DB 3; 100.0%; Pred. No. 32; tive 0; Mismatches
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                                      Length 569;
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; LOCATION: (1)...(569)
US-08-470-335-44
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                                                                        TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THE TITLE OF INVENTION: PREPARATION AND USE FILE REFERENCE: 04585/00200L

CURRENT APPLICATION NUMBER: US/08/735,021B

CURRENT FILING DATE: 1996-10-22

EARLIER APPLICATION NUMBER: 08/472,065

EARLIER FILING DATE: 1995-06-06

EARLIER FILING DATE: 1995-03-24

EARLIER APPLICATION NUMBER: 07/965,173

EARLIER FILING DATE: 1992-10-23

EARLIER FILING DATE: 1992-10-23
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APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: WAREHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
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Matches
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CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08735021B Patent No. 6194377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/08470335F Patent No. 6147190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                APPLICANT: MINGHETTI, LUISA
APPLICANT: WATTERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STROOBANT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, TITLE OF INVENTION: PREPARATION AND USE FILE REFERENCE: 04585/00200B
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                            EARLIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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nes 16; Conserv
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                                     FILING DATE: 1992-10-23
APPLICATION NUMBER: 07/9
FILING DATE: 1992-09-03
APPLICATION NUMBER: 07/
FILING DATE: 1992-06-30
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                  07/907,138
                                                        07/940,389
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Pred. No.
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32;
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US-08-734-664A-44/c
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LENGTH: 569
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Best Local
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EARLIER FILING DATE: 1992-04-03
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM Compatible Pentium
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
                               FILING DATE: 03-APR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                         FILING DATE: 26-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GLIAL MITOGENIC FACTIFLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 187
                                                                             PRIOR APPLICATION DATA:
                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                            APPLICATION NUMBER: FILING DATE: 30-JUN
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 26-MA
                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq Version 2.0
                                                                                                                                             FILING DATE:
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APPLICATION NUMBER: FILING DATE: 10-APP
                                                                APPLICATION NUMBER:
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176 Federal Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen, Mario
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                                                                                              30-JUN-1992
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                  UK 91 07566.3
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                                                                07/863,703
                                                                                                               07/907,138
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; LOCATION: (1)...(569)
US-08-470-339-44
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                                                                            Query Match
Best Local S
Matches 16
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Matches 16; Conservation
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APPLICANT: STROOBANT, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: WARCHIONNI, MARK
                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 91 07566.3 GB EARLIER FILING DATE: 1999-04-10 NUMBER OF SEQ ID NOS: 226
                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 07/907,138
EARLIER FILING DATE: 1992-06-30
EARLIER APPLICATION NUMBER: 07/863,703
EARLIER FILING DATE: 1992-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
EARLIER APPLICATION NUMBER: 07/940,389
EARLIER FILING DATE: 1992-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE FILE REFERENCE: 04585/002008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHEN, MARIO S. APPLICANT: HILES, IAN
                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                       LENGTH: 569
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66 tggttttgcagtaggc 81
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103 TGGTTTTGCAGTAGGC 88
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                                                                            Local Similarity hes 16; Conserv
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REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 0451
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                                                                                            5.7%; Score 16; DB 4; 100.0%; Pred. No. 32;
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PCT-US95-06846A-44/c
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PCT-US94-05083C-177
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                                                                                                                                                                                                              Sequence 44, Application PC/TUS9506846A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                             APPLICANT: Goodearl, Andrew David; Stroobant, Paul; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; APPLICANT: Chen, Maio Su; Hiles, Ian TITLE OF INVENTION: Glial Micogenic Factors, Their TITLE OF INVENTION: Preparation and Use NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/028WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/059,022 FILING DATE: 06-May-93 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209, 204
FILING DATE: 08-MAR-94
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                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-MAR-PRIOR APPLICATION DATA:
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SOFTWARE: Wordper
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                                      STREET:
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CITY: Boston
    STATE:
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New York City
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                                    E: Felfe & Lynch
805 Third Avenue
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Search completed: February 13, 2002, 20:05:45 Job time: 18172 sec
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STRANDEDNESS: single;
TOPOLOGY: linear
PCT-US95-06846A-44
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/036,555

FILING DATE: 24-MAR-193

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/965,173

FILING DATE: 23-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/940,389

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/907,138

FILING DATE: 30-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/863,703

FILING DATE: 03-APRIL-1992

PRIOR APPLICATION DATA:

APPLICATION
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 44
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06846A
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,322
FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS: LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5250.5
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 5.
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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BF146443 YO16508 L1
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The Institute for Genomic Re 9712, Medical Center Drive, Tel: (301)-838-3529
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Email: nhlee@tlar
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H34451.1
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                                                                Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A., Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D., Kerlavad,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                           H34451 319 bp mRNA EST 13-MAR-1998 EST111406 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA end similar to Glucose transporter, mRNA sequence.
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                                                                     Email: cdnaelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html f Plate: H3037 row: C column: 03
Seq primer: -21M13 Reverse
High quality sequence stop: 595
POLYA=NO.
                                                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Other_ESTs: H3037C03-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG079217 595 bp mRNA
H3037C03-5 NIA Mouse 15K CDNA Clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Seq primer: M13 Reverse.
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/db_xref="ATCC (inhost):2005510"
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/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
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/note="Vector: pBluescript SK-; Site_11: EcoRI; Site_2: Bluescript SK-; Site_11: EcoRI; Site_2: Bluescript SK-; Site_11: EcoRI; Site_2: Bluescript SK-; Site_11: Bluesc
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9192 row: d column: 12
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National Institutes of Health, Mammalian Gene Collection
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                                                      High quality sequence start: 4
High quality sequence stop: 644.
Location/Qualifiers
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/organism="Mus
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clone is among a rearrayed set of 15,247 clones from 11
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%;
100.0%;
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Pred. No. 1.8e-14;
0; Mismatches 0;
  musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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IMAGE:3986651 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT BF120840

FEATURES

Query Match Best Local Similarity Matches 48; Conserv

Conservative

Score 48; pred. No.

Length 917

Mismatches

Indels

0,

Gaps

0;

COMMENT

JOURNAL

REFERENCE

AUTHORS TITLE

KEYWORDS SOURCE VERSION ACCESSION DEFINITION

ORGANISM

DЬ Qy

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ORIGIN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 ggctggggacccatcccctggctcctcatgtcagagatcttccctctgca 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 917)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BF140667
                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9259 row: a column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF140667 917 bp mRNA
601786917F1 NCI_CGAP_Lu30 Mu:
                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 605.
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50; Conservative
                                                                                                                            163
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                                                                                                                          D
                                                                                                                        MMTV-LTR enhancer; Cloned unidirectionally. Primer dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 263 c 277 g 214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d'
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                        /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; transgenic model WNT-1, expression drive
                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
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/lissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                /clone="IMAGE:4014605"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3986651"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:10979707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; July 100.0%; Pro 0;
17.0°;
100.08; F1
0;
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Pred. No. 1.8e-14;
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                       DB 11;
. 1.8e-13;
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IMAGE:4014605
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mer: Oligo
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Briones, M.R.,

Sao Paulo-SP,

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ACCESSION
VERSION
KEYWORDS
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BF774206
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ORIGIN
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                                                                                   DEFINITION
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Best Local S
Matches 44
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sequence.
BF742266
BF742266.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegraid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                 BF/42266 32/ bp mRNA
RC1-BTN0409-021000-012-e12 BTN0409
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BF774206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                          h 15.6%; s
Similarity 100.0%;
44; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                       GI:12069046
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                                                                                                                                                                                                                                                                                          Score 44; DB; Pred No. 1.
0; Mismatches
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hes 0;
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                                                                                   Homo
                                                                                 sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                 Length 440;
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                               RESULT 7
AA627408/c
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Best Local Similarity 100
Matches 41; Conservative
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.ludwig.org.br/scripts/gethtml2.pl?il=RCI&t2=RCI-BTN0409
-021000-012-e12&t3=2000-10-02&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 11
High quality sequence stop: 327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., C
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                                                           Mammalia; Eutheria; Primates; 1 (bases 1 to 358)
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                          AA627408
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                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                      Eukaryota; Metazoa; Chordata;
                                                                                                                                                 human.
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                   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
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PROTEIN. ;, mRNA

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RESULT 8
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center

Trimming: cross_match from University of Washingtion Genome Center

PHRAP Suite. Poly-T identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Polyadenylation: Based upon the
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Other_ESTs: 2820759.5prime
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                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:1147207"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLAM10402 row:
                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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/tissue_type="transitional cell papilloma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SaII; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2: ECORI; cDNA made by oligo-df priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                        /clone="IMAGE:4514200"
/clone_lib="NIH_MGC_93"
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                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:2820759"
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Best Local Similarity 100
Matches 41; Conservative
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Best Local Similarity
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                            BG749509 949 bp
602707648F1 NIH_MGC_43
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plate: LLAM9706 row: i column: 01
High quality sequence stop: 710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
mRNA sequence.
BG749509
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                      /tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
291 c 287 g 213 t
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a 221 c 211 g 163 t
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/db_xref="taxon:9606"
/clone="IMAGE:3903048"
/clone_lib="NIH_MGC_70"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information
                                                                                                      Unpublished (1999)
Other_ESTs: 2820759.3prime
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, M
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2820759.5prime NIH_MGC_7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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Plate: LLCM1681 row: p column:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/Clone_lib="NIH_MCC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: xhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
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/db_xref="taxon:9606"
/clone="IMAGE:4844411"
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100.0%;
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Pred. No.
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                                                                                                                                                                            Mammalian
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. 5.7e-10;
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                                                                                                                                                                            Gene Collection (MGC)
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IMAGE:2820759 5',
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BASE COUNT
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BG672321
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PCR PRimers
FORWARD: T3
BACKWARD: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 538)
Xiao,H.S., Han,Z.G., Zhang,F.X., Huang,Q.H., Lu,Y.J., Bao,L., Fu,G., Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G., Chen,Z. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                             This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                    Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
                                                                                                                                                                                                                                                                                                                Contact: Zhang Xu
                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                       Distinct gene expression profiles of rat dorsal root ganglion
                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                             Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                           Laboratory of Sensory System
                                                                                                                                                                                                                                                                                                                                                              induced by peripheral nerve axotomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                      xu.zhang@ion.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lung; Vector: pOTBB; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_7"
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Pred. No. 0.00017;
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RESULT 1
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Best Local
Best Local Similarity
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                                                                                                                                                                                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
Plate: 70 row: A column: 21
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahrenkrug, S.C., Stone, R.T., Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia;
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EST.
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136437 MARC 1PIG Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrota
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                                                                                 /note="Vector: pCMV SPORT6; Site_1: Xbal;
Library made from pooled tissue from day 1
Library made from pooled and 30 embryos;"
and 30 embryos;"
182 c 162 g 124 t 2 others
                                                                                                                                               /clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                  Location/Qualifiers
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146 c 138 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Sprague-Dawle
/db_xref="taxon:10116"
                                                                                                                                                                                                   /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="dorsal root ganglion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Rat DRG Library"
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                                                                                                                                                                                                                   /organism="Sus scrofa"
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heaton, M.P.,
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100.0%;
9.6%;
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on,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
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 Score :
                                                                               162 g
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 DB 10;
0.0054;
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               Length 546;
                                                                                                                  _1: XbaI; Site_2: from day 11, 13, :
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REFERENCE
AUTHORS
TITLE
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SOURCE
CORGANISM
Search completed: February 13, 2002, 18:48:39 Job time: 18651 sec
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AL565390/c
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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http://fulllength.invitrogen.com"
a 206 c 242 g 118 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onote-"Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the
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/db_xref="toxon:9606"
/clone="CS0DF005YE02"
/clone_lib="LTT_FL013_FBrn1"
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/dev_stage="pooled tissue from post conception fetuse 
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

AUTHORS TITLE	REFERENCE	MEDLINE		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 HSA245937
Ibberson, M.R. Direct Submission	2 (bases 1 to 1873)	J. Biol. Chem. 275 (7), 4607-4612 (2000) 20138191	central nervous system and insulin-sensitive tissues	GLUTX1, a novel mammalian glucose transporter expressed in the	Ibberson, M., Uldry, M. and Thorens, B.	1 (bases 1 to 1873)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	glucose transporter; GLUTX1 gene.	AJ245937.1 GI:7018305	AJ245937	Homo sapiens mRNA for glucose transporter (GLUTX1 gene).	HSA245937 1873 bp mRNA PRI 18-FEB-2000	

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AFGAYEKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGNWCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
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/db_xref="GI:7018306"
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CSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSC
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CSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVARPVY1SELAYPAVRGLLGSC
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Transporters and ion channels
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Incyte Genomics, Inc. (US)
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Submitted (16-JUL-1998) H. Joost,
Toxicology, Technical University
Aachen, FRG
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Y17801
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Nachen, Wendlingweg 2, D-52057
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Norway rat.
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Eukaryota; Metazoa; Ch
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AJ245935
AJ245935.1
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Ibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammalian glucose transporter
central nervous system and insulin-sensitive t
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                              and
                                                                                                                                                       Direct Submission Submitted (02-SEP-1999) Ibberson
                                                                                                                                                                             Ibberson, M.R
                                                                                                                                                                                                                                                             Rattus
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                                                                                                                                              Toxicology,
                                                                                                                                                                                                                                                                                                                                             norvegicus
/gene="GLUTX1"
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/translation="MSPEDPQETQPLLRSPG/
                                                                                /db_xref="taxon:10116"
30. .1466
                                                                                                                                      SWITZERLAND
                                                             /gene="GLUTX1"
30. .1466
                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                          Location/Qualifiers
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Eutheria; Rodentia;
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                                                                                                                                              Son M.R.,
Lausanne,
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                              transporter
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                                                                                                                                                                                                                    tissues
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355 ø GYSSPAIPSLRRTAPPALRLGDTAASWEGAVVTLGAAAGGVLGGWLLDRAGRKLSLLL
CTVPFVTGFAVITAARDVMMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLGSC
VQLMVVTGILLAYVAGWVLEWRMLAVLGCVPPTLMLLLMCYMETPRFELLTQHGYQEA
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IPWLLMSEIFPLHIKGVATGVCVLTNMFMAFLVTKEFNSIMEILRPYGAFWLTAAFCI LSVLFTLTFVPETKGRTLEQITAHFEGR" 673 O 580 9

1184;

Conservative

0;

Score 1033.8; I Pred. No. 2.2e-0; Mismatches

DB 153; 207; 10;

Indels Length

6;

Gaps

2

Similarity

57.0%; 84.8%;

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TITLE
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Doege, H., Schurmann, A., Bahrenberg, G., Brauers, A. and Cordan Mariana (base)
                                                                                                                                                        Submitted (16-JUL-1998) H.
                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                             GLUT8, a novel member of the sugar transport with glucose transport activity
                                                                                                                                                                                     Joost, H.G.
                                                                                                                                                                                                      20283667
                                                                                                                                                                                                                                                                                                                             glucose transporter house mouse.
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/db_xref="taxon:10090"
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26. .1459
/codon_start=1
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Best Matches 1187; Query Match

Local

Similarity

56.7%; 85.0%;

Score 1027.4; Pred. No. 2.5e. 0; Mismatches

es 201; DB

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ccatctttgaagaggccaagttcaaggacagcctggcctcggtcgtcgtggtgtca
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Mus musculus
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AF232061.1 G
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Carayannopoulos, M.O., Chi, M.M., Cui, Y., Pingsterhaus, J.M., McKnight, R.A., Mueckler, M., Devaskar, S.U. and Moley, K.H. GLUT8 is a glucose transporter responsible for insulin-stiglucose uptake in the blastocyst
Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7313-7318 (2000)
                                                                                                             Proc. Nat
20319023
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Moley, K.H., Carayannopoulos, M.O.
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1187; Conservative
tctccctgatggccttccagcagctgtcggggggtcaacgccgtcatgttctatgcagaga
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Sequence
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Thorens, B., Ibberson, M. and Uldry, M.
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351 PWILMSEIFPLHVKGVATGICVLTNMFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL SVLFTLTVVPETKGRTLEQVTAHFEGR"

1 673 C 584 g 464 t GYSSPAIPSLRRTAPPALRLGDNAASWFGAVVTLGAAAGGILGGWLLDRSGRKLSLLL
CTVPFVTGFAVLTAARDVWMLLGGRLLTGLACGVASLVAPPYISESIAYPAVRGLLGSC
VQLMVVTGILLAYVAGWLEWRWLAGVLFTLMLLMCYMPETPRFLLTQHQYQEA
MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIGISLMVFQQLSGVNAI
MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAMLAVGSMCLFIAGFAVGWGPI

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56.5%; 84.8%;

Score 1024.2; DB 6 Pred. No. 7.2e-152; Mismatches

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                                                                                                                                                                                                                                                                                    MMU245936 2072 bp mRNA ROMUS musculus mRNA for glucose transporter AJ245936 1 GI:7018606 glucose transporter; GLUTX1 gene.
                                                                                                                      Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne,
                                                                                                                                                                                     GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2072)
                                                                                                                                              Direct
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                                                                                                                                                                    (bases 1 to
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56.5%; 84.8%;

0; Score Pred.

Mismatches

Indels

Gaps

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1024.2; DB 10; Length No. 7.2e-152; 203;

2072; 9;

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VERSION
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SOURCE
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DEFINITION
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                                                          Direct Submission Submitted (08-OCT-1999) to the DDBJ/EMBL/GenBank databases. Kenichi Ishibashi, Jichi Medical School, Pharmacology; Minami-kawachi, Kawachi, Tochigi 329-0498, Japan (E-mail:Kishiba@jichi.ac.jp, Tel:81-285-58-7326, Fax:81-285-44-5541)
                                                                                                                                                                                                              AB033418.1 GI:7592743
glucose transporter 8.
Rattus norvegicus cDNA to mRNA,
Rattus norvegicus
                                                                                                                   Molecular cloning of a new Published Only in DataBase 2 (bases 1 to 2189) Ishibashi, K.
                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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glut8
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Rodentia;
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(2000) In press
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Sciurognathi; Muridae;
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Similarity 84.6
34; Conservative
                       56.3%;
84.6%;
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                      Score 1020.8; DB Pred. No. 2.4e-151
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                Indels
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                9;
               Gaps
65
                w
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Qy

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VERSION
KEYWORDS
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DEFINITION
                                                                                                                                                                            RESULT 1
AX191507
                                                FEATURES
                                                                                               REFERENCE
                                                                                                                               SOURCE
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                                                                              AUTHORS
TITLE
                                                                                                                      ORGANISM
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                                                                                                                                            Ax191507
Sequence 29
Ax191507
Ax191507.1
                                                                                     Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (Dases 1 to 1461)
Kato,S. and Kimura,T.
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                                                                                                                      Homo sapiens
                                                                               proteins
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                                                                                                                                                                                                                           1396
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                                                     SAGAMI CHEMICAL
       protein
                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
       product'
                                                                              domains
                                                     RESEARCH CENTER
                                                                             and
                                                                                                     Hominidae;
                                                                             dnas
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                                                                             encoding
                                                                                                             Euteleostomi;
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a 501 c 456 g 309 t
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47.28; 74.78;

Length

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Local Similarity nes 1335; Conserv tgctgttcacagctgtggcggctctcatcatggacagagcagggcggaggctgctcctgg cggtctacatctccgaaatcgcctaccccagcagtccgggggttgctcggctcctgtgtgc tgctgctggggggccgcctcctcaccggcctggcctgcggtgttgcctccctagtggccc TGTGCTCCGTGCCCTTCGTGGCCGGCTTTGCCGTCATCACCGCGGCCCAGGACGTGTGGA tgtgctccgtgcccttcgtggccggctttgccgtcatcaccgcgggcccaggacgtgtgga CGGGGGGAGTGCTGGCGGCTGGCTGGACCGCGCGGGCGCAAGCTGAGCCTCTTGC cggggggagtgctgggctggctggtggaccgcgcgggcgcaagctgagcctcttgc CGCGCCTGGACGACGCCGCCGCCTCCTGGTTCGGGGCCTGTCGTGACCCTGGGTGCCGCGG cgcgcctggacgacgccgccgcctcctggttcggggctgtcgtgaccctgggtgccgcgg geggeegeegettetteetegeegeettegeegetgeeetgggeeeacteagettegget tgatggccttccagcagctgtcgggggtcaacgccgtcatgttctatgcagagaccatct ttcacctggccctgctgcggcagcccggcatctacaagcccttcatcatcggtgtctccc ggttcctgtggggctccgagcagggctgggaagacccccccatcggggctgagcagagct CGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGCTCGGCTCCTGTGTGC TGCTGCTGGGGGGCCGCCTCCTCACCGGCCTGGCCTGCGGTGTTGCCTCCCTAGTGGCCC Conservative Score 855.4; Pred. No. 2.7e 0; Mismatches 0, 1; DB 6; 2.7e-125; 1es 2; Indels 449; Gaps 605 425 845 725 707 664 545 604 485 544 484 365 424 305 364 304 185 244 65 707 707 707 245

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                       COW
    Metazoa;
                                                     glucose
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                                           se transporter
  Chordata;
  Craniata;
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                                                    (Glut8)
Vertebrata;
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A82; Conservative
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ttgtcaggtgtggttcatggtgttcagcacgagtgccttcggcgcctacttcaagctgacc
                                           CTGTTCACTGCCACGGCGGCCCTGATCATGGACAGAGCTGGGCGAAGGCTGCTCTTGACC
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Submitted (13-NOY-2000) Anatomy and Cell I
Medicine, Martin Luther University Halle,
Halle 061097, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
1 (bases 1 to 1012)
Augustin,R., Navarrete-Santos,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.
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/product - glucose transporter 8"

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LETATAALIMDRAGRRLLTLGSGVVMVFSTSAFGTVFKLTEGGPSNSSHVDLPALVSM

EAADTNVGLAWLAVGNMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGVCVLTNNP

MAFLVTKEFSSLMEVLRPYGAFWLASAFCIFGVLFTLACVPETKGKTLEQITAHFEGR
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<1. .1012
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<1. .1005
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87.3%;
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Pred. No. 7.9e-114;
0; Mismatches 122;
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Protegene Inc. (JP); SAGAMI CHEMICAL
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M1 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers giver in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP databases can be found at
                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 26, 2001 this sequence version replaced gi:13277497.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL445222
AL445222.
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp
                                                                                                                                                                                                                                                                                                                                               together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission {\sf var}
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Further information can be found at
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                                                                                                                            GTTTGCCAAATAAAGAC-TGACACAGAAAATCA 63462
                                                       RP11-356B19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-356B19 The true left end of clone RP11-373J8 is at 96439 in this sequence. The true right end of clone RP11-225021 is at 9980 in this sequence.
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/note="Single clone region. Sequence from reads from short insert library derived from a single pUC clone Restriction digest data confirm the assembly." 57092 c 57267 g 54682 t
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98.1%;
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Pred. No. 2.8e-77;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1813
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## ALIGNMENTS

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Nucleotide sequenc Aspergillus oryzae Rat glucose transp Human lung tumor a

Streptomyces roseo Human adenosine Al Total DNA sequence S. aureofaciens DN

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RESULT
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27-AUG-1999;
23-FEB-2000; 2;
13-JUL-2000; 2;
                                                                                                                                                                                              Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; SS; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                      Human GLUTX1 coding sequence.
                                                                                                                                                                                                                                                                                             AAF55865 standard; cDNA; 2217 BP
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SUMMARIES

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1024.2 855.4 346.4 327 237.2 150.6 137.4 125.6

97.6 97.0 57.0 56.5 47.2 19.1 18.0 13.1 8.3 7.6

2217 2080 2087 2072 1461 1541 1521 1527 1577

22 22 22 22 22 22 22 21 21 20

AAD12574 AAF55870

AAF55871 AAZ11731

AAA44914 AAZ32195

Human transport-as

WPI; 2001-112615/12. P-PSDB; AAB66932.

Rat GLUTX3 coding

Human secreted pro Corn hexose carrie

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disorders -
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14-JAN-2000;
21-JAN-2000;
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                                                        The present sequence is transporter and ion channel-1 (TRICH-1) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disease, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, pick's disease, Hintington's disease, stroke, cerebral neoplasms, pick's disease, Hintington's
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                    muscle
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and Parkinson's disease, demyelinating diseases, mental disorder ng mood, anxiety, Schizophrenia and seasonal affective disorder, disorder norder, myocarditis, polymyositis, myositis, arrhythmias and asthma and immunological disorders
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probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodi and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosi rheumatoid arthritis and insulin-dependent diabetes), to modulate

sclerosis

antibodies

The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA and the control of the complementary sequences may also be used as DNA and the control of the complementary sequences may also be used as DNA and the control of the contro

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03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
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RESULT
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ID AAF5
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AC AAF5
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DE Huma
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Huma

17-APR-2001

(first

entry)

AAF55870 standard; cDNA; 1541

ВP

6

Human GLUTX3

GLUTX; gene therapy; vaccine; coding sequence

hexose transport modulator;

	57 aggrgc	Db 13
aggtgcttttggaggttgggtgctgggcattcagtcgctcctctcacgcgggctgcctta	J	
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actaaagcagcggaagaggaggtgggcctct	cgcaa	Qy 16
ctctgaggactcaggaacaccttcgagctttgcagacctgcggtcagccc	37 tgctgci	Db 12
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ccagaatccagcccttggagccttggtctgcagggtccctc	46 agggga	QY 14
ggggatggagcaagcctgtgactccaagctgggcccaagcccagagcccctgcctg	57 ggggat	Db 10
- 10	86 ggggat	ОУ 13
aggaaagactctggaacaaatcacagcccattttgaggggcgatgacagccactca	97 aaggaa	Db 9
gactctggaacaaatcacagcccattttgaggggcgatgaca	26 aaggaa	Оу 13
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tctgcatcttcagtg	66 ttgcct	Оу 12
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ctgttgatgccagcgtgggctggcctggctggccgtgggcagcatgtgcctcttcatcg	43 ctgttg	Db 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3;
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27-AUG-1999;
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13-JUL-2000;
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hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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DB; AAB66937.
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23-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents human transport-associated protein-1 (TRANP-1) cDNA. The DNA sequence was first identified in a human colon tissue cDNA library. The full-length cDNA was derived from a series of overlapping and/or extended cDNA sequences and is a consensus.

TRANP-1 to 9 (AAY31639-Y31647) are a novel group of proteins with chemical and structural homology that are involved in molecular
                                                                                                                                                                                                                                                                                                          the adrenal medulla can secrete excessive amounts of adrenaline and noradrenaline, leading to hypertension. TRANP is expressed in cancer cells, and transport disorders result from either excessive or
                                                                                                                                                                                   insufficient molecular transport. Anti-TRANP antibodies and nucleic acids encoding TRANP can be used as diagnostic tools for such disorders. TRANP antagonists can be used to treat or prevent a cancer associated with increased TRANP expression. Anti-TRANP antibodies can be used directly
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                                                             antagonist or as a targetting mechanism for drugs. Alternatively, RANP antisense nucleotide can be used to treat cancers. A TRANP st or expression vector may be used to treat a disorder caused by ed transport of biologically active molecules.
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21-AUG-2000

(first entry)

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Query Match
Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags (sESTs), isolated from human, mouse, chicken a tissue sources. The sESTs can have a range of activities dependent the tissues they were isolated from The activities include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
                                                                                                                                                                                                                                   disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression psoriasis. AAA45926 to AAA45931 represent linker variants which are in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                            (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA43426 to AAA45925 represent specifically claimed secreted expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merberg D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC
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immunomodulatory; haematopoietic; chemokinetic; analgesic;
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                            8.3%;
94.5%;
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   0;
                                Score 150.6; DB:
Pred. No. 2.4e-20
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       Mismatches
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                                                             DB 21;
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                                                                                                                                                                         other;
   Indels
                                                             Length 579;
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                                                                                                                                                                                                                                                                                                           depression and
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                                                               cerebrovascular disorders e.g. cerebral ischaemia, ängiogenesis, nerv
system disorders e.g. Alzheimer's disease, infections caused by
bacteria, viruses and fundi and ocular disorders e.g. corneal infecti
The polypeptides can also be used to aid wound healing and epithelial
                                                                                                                                                                    e.g. rheumato1d arthitts, "Irreference disorders e.g. cardiac art of the breast or liver, cardiovascular disorders e.g. cardiac art
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent alternative polypeptides encoded by the genes, and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073
cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary
                                                                                                                                                                                                                                                                                                                       fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or \,
                                                                                                                                                                                                                                                                                                                                                                                                                                of their activities include immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -  \frac{1}{2} \sum_{i=1}^{n} \frac{1}{2} \sum_{i=1}^{
                                                                                                                                                                                                                                                                                     diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                          cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC80569 standard; cDNA; 1577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 CTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGTG 202
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                                                                                                                                                                                                                                                   rheumatoid arthritis, hyperproliferative disorders
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99US-0172410
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ID AAZ321
XX AAZ321
XX AZ321
XX 11-JAN
DT 14-JAN
XX Hexose
KW Carboh
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-080530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of
                                                                              carbohydrate carbohydrate
                                                                                                                                    Corn hexose carrier protein
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  21-OCT-1999
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                                                      Zea mays
                                                                                                            Hexose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 gacgcagccatcgttggggccgtgcggctcctgtccgtgctgatcgccgccctcaccatg
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                                                                              carrier protein; corn; rice; sydrate transport; plant carbon ydrate distribution; ss.
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No. 9.8e-18;
smatches 226; Indels
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Matches 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carrier proteins may be used to manipulate carbohydrate transport a alter whole plant carbon partitioning or to manipulate carbohydrate distribution between cellular compartments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes part of a hexose carrier protein from the invention, which describes hexose carrier proteins isolated from sorghum rice, wheat, soybean and corn. Also describes are: (1) a chimeric gene
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                                    aagaccccccatcggggctgagcagagctttcacctggccctgctgcggcagcccggca
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-catccgcggcacggacgacatcggcgaggagtacgcggacctggtggcggccagcg
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Pred. No. 1.9e-15;
0; Mismatches 564;
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24 - AUG - 1998;
24 - AUG - 1998;
09 - SEP - 1998;
28 - SEP - 1998;
25 - NOV - 1998;
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                                                                                                                                                                                                                                                                                  Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflam infection; fungal; bacterial; viral; HTV; allergy; arthritis;
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                                                                                                                                                                                                                                                                                                                                            cDNA encoding human secreted protein vql_1,
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98US-0097659.
98US-0099618.
98US-0102092.
98US-0109978.
                                                                                    99WO-US19351
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                                                                                                                                                                    /*tag= a
/product= "Human secreted protein vql_1"
                                                                                                                                                                                   /*tag=
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inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain Barre syndrome; insulin dependent diabetes mellius; and allergic reactions such as insulin dependent diabetes mellius; and affects the second of the second o
                                                                                                       asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haem and thrombolytic activity; anti-inflammatory activity; and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine activity; cell proliferation; differentiation; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 86; Page 335; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
Sequence 823
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BP; 170 A;
                                                                       of the 40 proteins of the invention.
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99US-0379246.
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   257 C;
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233 G; 163 T; 0 other;
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or

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Matches 191;
               Query Match
         Best
       Local Similarity
Conservative
       6.8%;
0;
       Score 123.8;
Pred. No. 3.7
Mismatches
        .7e-15;
                DB 21;
112;
Indels
                Length 823;
0;
Gaps
0;
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Qy Db Qy Db QУ DЪ γ QУ 1106 207 147 87 27 gggcccatcccctggctcctcatgtcagagatcttccctctgcatgtcaagggcgtggcg 1165 ttcagtgtccttttcactttgttctgtgtccctgaaactaaaggaaagactctggaacaa agcctcatggaggtcctcaggcctatggagccttctggcttgcctccgctttctgcatc acaggcatctgcgtcctcaccaactggctcatggcctttctcgtgaccaaggagttcagc ctcaccctggtgcccctgctggccaccatgctcttcatcatgggctacgccgtgggctgg ccagtggtgagcaccttcggcctccaggtgcctttcttcttcttcgcggccatctgcttg ggtcccatcacctggctgctcatgtctgaggtcctgccctgcgtgcccgtggcgtggcc 1105 86

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atc 1348

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gtgagcctggtgttcacaggctgctgtgtgcccgagaccaagggacggtccctggagcag

326

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RESULT 1
AAF67134
ID AAF6
XX AAF6
XX AAF6
XX NOVE
XX NOVE
XX HUMBA
KW BTEE
XX HOMC
XX WPI.
XX Cla:
XX WPI.
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Best Local S
Matches 188
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Reinhard C, R
Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                      1113
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                               preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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breast cancer; lung
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tcacctggctgctcatgtctgaggtcctgcccctgcgtgcccgtggcgtggcctcagggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  f polynucleotides for diagnosing a cancerous state of cell and detecting cancer, particularly of the colon comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Randazzo F, F, Drmanac S,
                                                                                                                                                                                                                                                                                                                   ₿P;
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g cancer; cancer detection; ss.
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Kennedy GC, I
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LW, Strach
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                                                                                                                                                                                            Score 123.2; DI
Pred. No. 4.2e-
0; Mismatches
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Leshkowitiz
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1173
                                                                                                                                                                                     treatment and
                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
21-JAN-2000;
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dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory;
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                                                                                                                                                                                                     Isolated
                                                                                                                                                                                                                                                                                                        (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein
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DB; AAM25722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; ulcer; HIV infection; human
                                                                                                                                                                                                                                                                                                        HYSEQ
                                                                                                                                                                                     human polynucleotides encoding polypeptides, useful t and diagnosis of e.g. cancer, ulcers and HIV infect
                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                     99US-0471275.
2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic;
                                                                                                                                                                                                                                                                               Drmanac
                                                                                                                                                                                                                                                                               RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion; human immunodeficiency virus;
antiarthritic; immunosuppressive;
                                                                                                                                                                                        and HIV infection
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antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides

be

used in gene

therapy,

antisense

cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and

Claim 1;

Page 564; 1217pp; English

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RESULT 1
AAT66495
ID AAT6
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Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                    Use of glucose transporter, GLUT-2 or GLUT-2 chimera(s) for cell-killing - used in negative and double selection protocols and screening methods, for cancer treatment and treatment of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1175
           Claim 138; Page 104-106;
                                                                                                                                                                                                                                                                                                                                                                                                                           Glucose transporter; GLUT-1; GLUT-2; chimeric transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human glucose transporter GLUT-1 cDNA
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                                                                                                                                    Clark SA,
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                                                                                              P-PSDB; AAW17835
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                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                               BETAGENE INC
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                                                                                                                                   Newgard CB,
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165..1643
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71.4%;
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No. 6.2e-09;
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                                                                                                                                   Thigpen
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Best Local S
Matches 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA sequence codes for human glucose transporter GLUT-1 (AAM17835). A claimed polyrucleotide comprises a contiguous nucleic acid sequence from human GLUT-1 cDNA and rat GLUT-2 cDNA (see AAT17835). It encodes a GLUT-1/GLUT-2 chimeric transporter that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1815 BP; 324 A; 572 C; 520 G;
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TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1993US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
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Pred. No. 1e-06;
0; Mismatches 329;
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126 ogcgcctggacgacgccgcctcctggttcggggctgtcgtgaccctgggtgccgcggg 185

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Best Local
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application
         20412
                                                                                                                                                                                                                                         TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Tsevdos, Estelle J
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                    Local Similarity
mes 264; Conserv
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 22-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                     gcggccgcgcgtcttcctcgccgcttcgccgctgccctgggcccactcagcttcggct
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One Cyanamid Plaza
                                                                   Conservative
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VENVION: Cloning of the biosynthetic pathway for VENTION: chlortetracycline and tetracyline Formation and cosmids
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                                                              Score 67.8; DB 1;
Pred. No. 3e-05;
0; Mismatches 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of
TITLE OF INVENTION: Cloring of
TITLE OF INVENTION: useful the
             TELEFAX: (201)831-330
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                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                        TELECOMMUNICATION INFORMATION:
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CITY: V
STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
                                                      TELEPHONE:
                                                                                       REFERENCE/DOCKET NUMBER: 31,145
                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                            NAME: Tsevdos, Estelle J
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
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                                                    (201)831-3241
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Matches
                               SOFTWARE:
SEQ ID NO 8
                                                                                                                                                                                                                                                                                Sequence 8, Application US/09591025 Patent No. 6303373
                                                                                                                                                                              APPLICANT: Bogan, Jonathan S.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Method of Measuring
TITLE OF INVENTION: Targeting of GLUT4
FILE REFERENCE: 0399.1210-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-(
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-(
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/591,025
CURRENT FILING DATE: 2000-06-09
                                                                NUMBER OF SEQ ID NOS:
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TYPE: DNA
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1999-09-15
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Patent No. 6114111
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Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHAX: (415) 949-8711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
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                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                  CLASSIFICATION:
                                                                                                                                     FILING DATE:
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                    SOFTWARE:
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; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-050-863-2
                                                                                                                                                                                                                                                      US-09-130-114-1
US-09-130-114-1
                                        SEQ ID NO 1
LENGTH: 5452
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
                                                                                                                                                                                                                         Sequence 1, Application US/09130114 Patent No. 5976807
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Best Local Similarity
                                                                                              CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                         TITLE OF INVENTION: Eukaryotic Cells Stably Expressing TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/1D903US1
                                                                                                                                                                  APPLICANT: Damaj, Bassam B. APPLICANT: Robbins, Alan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                    SOFTWARE: FastSEQ for Windows Version
                                                                                  NUMBER OF SEQ ID NOS:
             ORGANISM: VEBNA
                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tccgaaatcgcctacccagcagtccgggggttgctcggctcctgtgtgcagctaatggtc
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Query Match 3.3 Best Local Similarity 45.7 Matches 207; Conservative

3.3%;

Score 59.4; DB 2 Pred. No. 0.0011; 0; Mismatches 24

DB 2;

Length 5452;

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; TOPOLOGY: 1i; MOLECULE TYPE: US-08-910-647-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                           TELEFAX: (510) 655-354
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 cagcagctgtcgggggtcaacgccgtcatgttc
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                                              STRANDEDNESS:
                                                                                                                                                                           NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                              LENGTH:
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VENTION: Compositions and Methods
VENTION: Polynucleotide Delivery
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RESULT 9
US-07-884-811-15/c
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Best Local
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                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                          TELECOMMUNICATION INFORMATION:
                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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CITY: South San Francisco
STATE: California
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                                                           NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                           FILING DATE
                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 199205
                                                                                                                                                                                                                                                    COMPUTER:
             TELEPHONE:
                                              REFERENCE/DOCKET NUMBER:
                                                                                                                          APPLICATION NUMBER:
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Similarity 45.78;
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: 415/225-3216
415/952-9881
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Pred. No. 0.0012;
0; Mismatches 24
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RESULT 10
US-07-885-971-15/c
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                     Sequence 15, Application US/07885971 Patent No. 5328837
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                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                              OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                        2603
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               TITLE OF INVENTION:
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           APPLICATION NUMBER: FILING DATE: 19920 CLASSIFICATION: 53
                                                                                                                                                             STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                    CTGCCCCTCCTGCCCCTCCTGCTC
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                                                                                                                                                                                                                                             HEPATOCYTE GROWTH
                                                                             PC-DOS/MS-DOS
                                       US/07/885,971
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                                                                                                        360 Kb floppy
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RESULT 11 US-08-087-783A-15/c

Sequence 15, Application US/08087783A Patent No. 5547856

GENERAL INFORMATION: APPLICANT: Godows

APPLICANT: GOdowski, Paul J., Lokker, Nathalie A., Ma: TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS

Mark,

Melanie

CORRESPONDENCE ADDRESS

ADDRESSEE:

Genentech,

STREET: 460 Point San Bruno CITY: South San Francisco STATE: California

COUNTRY: US ZIP: 94080

USA

NUMBER OF SEQUENCES:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible

floppy

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Best Local Similarity 45.7%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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2603 CTGCCCCTCCTGCCCCTCCTGCTC
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
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STRANDEDNESS: single
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                      cagcagctgtcgggggtcaacgccgtcatgttc
                                                          ctgctgcggcagcccggcatctacaagcccttcatcatcggtgtctccctgatggccttc 736
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415/952-9881
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CURRENT APPLICATION DATA:

OPERATING SYSTEM: SOFTWARE: WinPat.

WinPatin

PC-DOS/MS-DOS

(Genentech)

US/08/087,783A

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RESULT 12
US-08-194-088B-15/c
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                                                Sequence 15, Application US/08194088B Patent No. 5580963
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Best Local Similarity
Matches 207; Conserv
 GENERAL INFORMATION:
APPLICANT: Godowski,
TITLE OF INVENTION:
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TELEPAN: 415/52-981
TELEPAN: 700 CRET NUMBER: P075.
TELEPHONE: 415/225-5416
TELEPAN: 415/952-9881
TELEPAN: 415/952-9881
TELEPAN: 910/371-7168
INFORMATION FOR CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                   2843
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ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    497
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCCCCTCCTGCCCCTCCTGCCCCTCCTGCTC 2571
                                                                                                                                                                                                                ctgctgcggcagccggcatctacaagcccttcatcatcggtgtctccctgatggccttc
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, Paul J. Lokker, Nathalie A. SINGLE-CHAIN HEPATOCYTE GROWTH
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Pred. No. 0.0013;
0; Mismatches 246; Indels 0;
 Mark, I
 Melanie R
R VARIANTS
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                                                                                                                                                                                                                                                                                                           2903
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
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PRIOR APPLICATION DATA:
07/884811
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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CURRENT APPLICATION DATA:
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Local Similarity 45.7%;
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                    cagcagctgtcgggggtcaacgccgtcatgttc 769
                                                                            ctgctgcggcagcccggcatctacaagcccttcatcatcggtgtctccctgatggccttc 736
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CTGCCCCTCCTGCCCCTCCTGCTC 2571
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Pred. No. 0.0013;
0; Mismatches 246; Indels
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Godows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                        2783
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                                                                                                                                                                                                                                                                                      3023
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                            617
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                                                                                                                                                                                                                                                                                                            317 ggccgcctcctcaccggcctggcctgcggtgttgcctccctagtggccccggtctacatc 376
                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                       ccgcgcttcctgctgactcagcacaggcgccaggaggccatcgccctgcggttcctgtgg 616
                                                                                                            gtgctggggtgcccccctccctcatgctgcttctcatgtgcttcatgcccgagacc
                                                                                                                                                                     GGCGGCCTCCACTACCTCCTCGACCCCGGCCTCCACTACCTCCTCGACCCCGGCCTCCAC
                      ggctccgagcagggctgggaagacccccccatcggggctgagcagagctttcacctggcc 676
                                                     TGCCTCCTCGACCCGGCCTCCACCTCCTGCTCCTGCCCCTCCTGCCCCCTCCTC
                                                                                                                                                                                                                                                      tocgaaatogcotaccoagcagtocgggggttgctocggctoctgtgtgcagctaatggto 436
                                                                                                                                                                                                                                                                                                                                              207;
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South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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415/952-9881
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                          3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ., Paul J. Lokker, Nathalie A. Mark, Melanie R. HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/194,087
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Pred. No. 0.0013;
0; Mismatches 246;
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application PC/TUS9304648 GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Godows
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            3023
                                                                                                              2963
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
FILING DATE: 18-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
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                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genentech, Inc., Godowski, Paul J., Lokker, TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2603 CTGCCCCTCCTGCCCCTCCTGCTC 2571
497 gtgctgggctgcgcccccctccctcatgctgcttctcatggctgcttcatggcccgagacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Ginger R
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                  tccgaaatcgcctacccagcagtccgggggttgctcggctcctgtgtgcagctaatggtc 436
                                                                                                                                                                            GGCGGCCTCCACTACCTCCTCGACCCCGGCCTCCACTACCTCCTCGACCCCGGCCTCCAC 2964
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                                                                                                            TGCCTCCTCGACCCGGCCTCCACCTCCTGCTCCTGCCCCTCCTGCTCCTCCTC
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                                                                                                                                                                                                                                        Conservative
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Pred. No. 0.0013;
0; Mismatches 246;
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TITLE OF INVENTION: Systematic Polypeptide Ever File Reperence: Nexo2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Sequence of HER INFORMATION: having a 120 repeat of ACG flanked by fixed to OTHER INFORMATION: fragments having NcoI restriction sites. US-09-197-649-7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                             Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pribnow, David APPLICANT: Smith, Jonathan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gold, Larry APPLICANT: Tuerk, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                  99accgcgccgggcgcaagctgagcctcttgctgtgctccgtgcccttcgtggccggctt 273
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                                                                                                               Conservative
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Search completed: February 13, 2002, 13:34:27 Job time: 2794 sec

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                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      February 13, 2002, 12:47:53; Search time 2842.4 Seconds (without alignments) 6854.101 Million cell updates/sec
                                                                                                                                                                                                                                                                      EST:*
                                                                                                                                                                                                                                                                                                                                                                                                         11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                              Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_gss_fun:*
em_gss_hum:*
em_gss_inv:*
em_gss_pin:*
em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                       em_htc:*
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                                                                                                                                                                                                         em_estpl:*
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gb_est2:*
em_gss_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	% Query Match	% Query Match Length	DB	В
۲	801.4	44.2	932	11	
2	768.6	42.4	949	11	BG749509
w	746.2	41.2	830	11	BG70074
4	701.6	38.7	991	11	81
c 5	659	36.3	752	10	AL5
6	634.8	35.0	828	11	BG478000
7	634.4	35.0	879	1	BG7
8	633	34.9	934	11	BE9
9	631	34.8	777	11	BG71703
10	603.6	33. 3	712	11	BG29017:
11	599	33.0	838	11	BG28177
12	499.2	77 5	801		271117

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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	1/	16	15	14	13
359.4	9									8	8	9									428.6	7		9	454.6	45	471	4/2	476	477	482.4	4.8
			•						•																			•	•			26.6
374	389	458	478	477	623	425	823	389	396	498	927	911	529	487	920	421	442	917	595	441	466	451	460	442	594	457	480	4/3	621	651	6//	664
10	10	10	10	11	10	10	11	10	10	11	11	11	11	10	11	10	10	11	11	10	10	10	10	10	11	10	10	LO	1	10	-	11
AW300979	AI970024	W49131	E11529		E2822	12902	BF120840	AL041348	A1025047	BI403682	BF207033	BF311341	BI404477	AA293722	BF308306	AI205662	AA436091	BF140667	BG079217	AI338697	AI149830	AI338005	AW055123	AW051497	B1402088	A1971919	AW249090	AI094911	BE986074	W95545	BG/0/10/	BE986058
		-IU	- II	BF400621 UI-R	BE282246 6011	AI290245 gm01	BF120840 6017	AL041348 DKFZ	AI025047 ov36	BI403682 MI-P	BF207033 6018	BF311341 6018	BI404477 MI-P	AA293722 zt55	BF308306 601890370	AI205662 qg31.	AA436091 zu03			AI338697 qt46	AI149830 qf32	AI338005 gt35	AW055123 wy99	AW05149/ wysowii								18:
xk10f10.x	)q10.x	м-внз-	R-CAO-	R-CA0-	601101202	a06.x	601757442	;p434P	b11.x	P-CP1-	370114	601896741	-CP1-	zt55h05.s	390370	a06.x	zu03a11.r	601786917	37C03-	e08.x	qf32e07.x	6d10.x	)h11.x	2							1	08

## ALIGNMENTS

	source	FEATURES								COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	100:00:0	RESULT 1
/organism="Homo sapiens" /db_xref="taxon:9606" /clone=_TMACE:465906" /clone_lib="NIH_MGC_21" /tissue_type="choriocarcinoma" /lab_host="DH10B (phage-resistant)"		night quality sequence stop: 620.  Location/Qualifiers	Plate: LLCM1433 row: a column: 19	found through the i.m.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Clone distribution: MGC clone distribution information can be	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Preparation: Ling Hong/Rubin Laboratory	Tissue Procurement: ATCC	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 932)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	7	human.	EST.	BG479842.1 GI:13412121	BG479842	602527373F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:4650906 5′,		

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Query Match
Best Local Similarity
926 gtgttcagcacgagtgccttcggcgcctacttcaagctgacccagggtggccctggcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 GACTCAGCACAGGCGCCAGGAGGCCATGGCCGCCCTGCGGTTCCTGTGGGGCTCCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 catccctagcctgcagcgcccgcgcccccggcccccggccctggacgacgccgccgcctc 150
                                                                        gctctcatcatggacagagcagggcggaggctgctcctggtcttgtcaggtgtggtcatg 925
                                                                                                                                                              acagcagcetgg-cctcggtcgtcgtgggtgtcatccaggtgctgttcacagctgtggcg 865
                                                                                                                                                                                                                                    CGGGGGTCAACGCCGTCATGTTCTATGCAGAGACCATCTTTGAAGAGGCCAAGTTCAAGG
                                                                                                                                                                                                                                                                                                                                                   agcccggcatctacaagcccttcatcatcggtgtctcccctgatggccttccagcagctgt 746
                                                GCTCTCATCATGGACAGAGCA-GGCGGAGGCTGGTCCTGG-CTGGTCAGGTGTGGCCATG
                                                                                                                                         ACAGCAGCCTGGCCCTCGGTCGTGCGTGTGTCATCCAGGTGCTGTTCACAGCTGTGGGG
                                                                                                                                                                                                                                                       cgggggtcaacgccgtcatgttctatgcagagaccatctttgaagaggccaagttcaagg
                                                                                                                                                                                                                                                                                                                        AGCCCGGCATCTACAAGCCCTTCATCATCGGCGTCTCCCTGATGGCCCTTCCAGCAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGCTGGGAAGACCCCCCCATCGGGGCTGAGCAGAGCTTTCACCTGGCCCTGCTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              agggctgggaagacccccccatcggggctgagcagagctttcacctggccctgctgcggc 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gactcagcacaggcgccaggaggccat---cgccctgcggttcctgtgggggctcc-gagc 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gccccctcctcatgctgcttctcatgtgcttcatgcccgagaccccgcgcttcctgct 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcctggcctgcggtgttgcctccctagtggccccggtctacatctccgaaatcgccta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctttgccgtcatcaccgcggcccaggacgtgtggatgctgctgggggggccgcctcctcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cccagcagtccgggggttgctcggctcctgtgtgcagctaatggtcgtcgtcgtcgtcgtct 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCCCCTCCTCATGCTGCTTCTCATGTGCTTCATGCCCGAGACCCCGCGCTTCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTGCCGTCATCACCGCGGCCCAGGACGTGTGGATGCTGCTGGGGGGGCCGCCTCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGGACCGCGGGGGCGCAAGCTGAGCCTCTTGCTGTGCTCCGTGCCCTTCGTGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 318 c 314 g 194 t
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96.78;
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Pred. No. 5e-114;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 932;
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                                                                                                                                                                               1003 ctcggcgcctgtctctgcacagcctgttgatgccagcgtggggttggcctggcctggccgt 1062
                                                                        121
                                                                                                                                                                                                                                                                        943 cttcggcgcctacttcaagctgacccagggtggccctggcaactcctcgcacgtggccat 1002
                                                                                                                                                              61
                                                                                                                                                                                                                                                  2 CTTCGGCGCCTACTTCAAGCTGACCCA-GGTGGCCCTGGCCAACTCCTCGCACGTGGCCAT 60
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Qy Дb

121

Дb Qy Ъ Qy

61

151

BASE COUNT ORIGIN

Matches

904;

δ В Qy В Qy В Qy Db 20 Вb Qy Дb QΥ B Qy DЪ δÃ Вb QY В Qy Вþ Qy

cctcatgtcagagatcttccctctgcatgtcaagggggtggggacaggcatctgcgtc

999cagcatgtgcctcttcatcgccggctttgcggtgggctgggggcccatcccctggct 112 GGGCAGCATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGGGGGCCCATCCCCTGGCT

CTCGGCGCCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGGGCTGGCCTGGCCGT

120

781

721 807 661747 601 541

571

421

361 451 301 391 241 331 181

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BASE COUNT
ORIGIN
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                                          Query Match
Best Local Similarity
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            827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCGC-CGTGGCCATCTCGGGCCTTGTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG749509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 949)
                                                                                                                                                                                                                                                        160
            Conservative
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/db_xref="taxon:9606"
/clone_"IMAGE:4844411"
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/tissue_type="normal pigmented"
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/tisue_type="normal epithelium"
/tissue_type="normal epithel
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NIH_MGC_43 Homo sapiens cDNA
                                              42.48;
96.88;
        0;
                                          Score 768.6; DB 11 Pred. No. 5.5e-109;
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        Mismatches
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        Indels
                                                                                Length 949;
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BG700749
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                                                                                                                                                                                                               AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGGGTCCCTCCTGTCATGCTCCCTCCAGCCCATGACCCGGGGCTAGGAGGCTCA 600
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                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                 BG700749 830 bp mRNA EST 602681616F1 NIH_MGC_95 Homo sapiens cDNA clone BG700749.1 GI:13970402 EST.
found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                       Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                      (bases 1 to 830)
                                                                                                                                                                       Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852
                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           Gene
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994 604

cgtggccatctcggcgcctgtctctg-cacagcctg-ttgatgccagcgtggggctggcc

catggacagagcagggcggaggctgctcctggtcttgtcaggtgttggtcatggtgttcag 933

CATGGACAGAGCAGGCGGAGGCTGCTCCTGGTCTGTCAGGTGTGGTCATGGTGTTCAG

603

cctggcctcggtcgtcgtgtgtcatccaggtgctgttcacagctgtggcggctctcat CAACGCCGTCATGTTCTATGCAGAGACCATCTTTGAAGAGGCCAAGTTCAAGGACAGCAG

873

483

543

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544

484 814 424 694

304

754 364

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423

363

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caacgccgtcatgttctatgcagagaccatctttgaagaggccaagttcaaggacagcag

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GCACAGGCGCCAGGAGGCCATGGCCCTGCGGTTCCTGTGGGGCTCCGAGCAGGGCTG
                                                                                                                                                  CTCCCTCATGCTGCTTCATGTGCTTCATGCCCGAGACCCCGCGCTTCCTGCTGACTCA
                                                                                                                                                                   ctccctcatgctgcttctcatgtgcttcatgcccgagaccccgcgcttcctgctgactca 576
                                                                                                                                                                                                                      agtccgggggttgctcggctcctgtgtgcagctaatggtcgtcgtcgtcggcatcctcctggc 456
                                                                                                                                                                                                                                                                                                                                                                       GGCCTGGGGTGTTGCCTCCCTAGTGGCCCCGGTCTACATCTCCGAAATCGCCTACCCAGC 63
                                                                                                                                                                                                                                                                                                                                                                                        ggcctgcggtgttgcctccctagtggccccggtctacatctccgaaaatcgcctacccagc 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site-1: BamHI; Site_2: SalI-XhoI(gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 271 c 266 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_95"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 746.2; DB 11;
pred. No. 1.6e-105;
0; Mismatches 18;
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TITLE
JOURNAL
                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                          Matches
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ctggagtggctgtggctgtggtgggtgcgcccctcctcatgctgcttctc
                                                                                                                                                                     catcccctggctcctcatgtcagagatcttccctctgcatgtcaagg
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                                                                                                               ctagtggccccggtctacatctccgaaatcgcctacccagcagtccgggggttgctcggc
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                                                  TCCTGTGTGCAGCTAATGGTCGTCGTCGGCATCCTCCTGGCCTACCTGGCAGGCTGGGTG
                                                                                                    TCCTGGCGGCAGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGCTCGGC
                                                                                                                                                      GGCGTTGGCCGCCGACATGACGCCCGAGGACCCCAGAGGAAACCCCAGCCGCTTCTGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCCCCTTGCTCCTCATGTCAGAGATTTTCCCTCTTGCTGTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BI334832
BI334832.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI334832 991 bp mRNA EST 30-JUL-2001 602998959F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM11347 row: f column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 991)
                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 835.
Location/Qualifiers
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                Technologies.
                                                                                                                                                                                                                                                                                                /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5141007"
/clone_lib="NIH_MGC_12"
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                                 Li,W.B., Gruber,C., Jessee,J. and Full-length cDNA libraries and nor Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de S
BP 191 91006 EVRY cedex - France
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                                                                          Mammalia; Eutheria;
1 (bases 1 to 752)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Petal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://fulllength.invitrogen.com"
206 c 242 g 118 t
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/lab_host="DH10B"

/note=""""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CS0DF005YE02"
/clone_lib="LTI_FL013_FBrn1"
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Plate: LLCM1407 row:
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Clone distribution: MGC clone distribution info
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, N
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/clone_lib="NIH_MGC_20"
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96.5%;
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                                                                                                                                                                                                                                                                             Score 634.8;
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AUTHORS
TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BG771736
BG771736.1 GI:
                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), $
cDNA Library Preparation: Michael J. Brownstein (NHGRI), $
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                             I (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG//11/36 879 bp
602720404F1 NIH_MGC_97
                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM10769 row: h column: 02
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                                                                                                                             quality sequence stop: Location/Qualifiers
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4837297"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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  5'-TTTTTTTTTTTTTTTVN-3',
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RESULT BE910478 LOCUS

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BE910478 934 bp 601501005F1 NIH_MGC_70

Homo

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Best Local :
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tgtctccctgatggccttccagcagctgtcggggggtcaacgccgtcatgt
                                                agctttcacctggccctgct--gcggcagcccggcatct--acaagcccttcatcatcgg
                                                                                TGCGGTTCCTGTGGGGCTCCGAGCAGGCTGGGAAGAACCCCCCATTCGGGGCTGAGCCAG
                                                                                              tgcggttcctgtggggctccgagcagggctgggaagacccccccatcgggggctgag-cag
                                                                                                                                                                                                                              AGCTAATGGTCGTCGGCATCCTCCTGGCCTACCTGGCAGGCTGGGTGCTGGAGTGGC
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                                   AGCTTTCACCTGGGCCCTGTTGCGGACAGCCCGGGATCTTACAGAGCCCTTCATCATCGG
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94.2%;
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Pred. No. 2.3e-88;
0; Mismatches 36;
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                                                                                                 cagcctgttgatgccagcgtggggctggccttggctggccgttgggcagcatgtgccttttc 1081
                                                                                                                                                                                   ctgacccagggtggccctggcaactcctcgcacgtggccatctcggcgcctgtctctgca 1021
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ATCGCCGGCTTTGCGGTGGGCTGGGGCCCATCCCCTGGCTCCATGTCAGAGATCTTC
                                                                                                                                                             CTGACCCA - GGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGGCGCCCTGTCTCTGCA
                                                                                                                                                                                                                                                CTGGTCTTGTCAGGTGTGGTCATGGTGTTCAGCACGAGTGCCTTCGGCGCCCTACTTCAAG
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Tissue Procurement: ATCC
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Plate: LLAM9706 row: i column: 01
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/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

291 c 287 g 213 t
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/db_xref="taxon:9606"
/clone="IMAGE:3903048"
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Pred. No. 3.7e-88;
D; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                Plate: LLAM10728 row: i column: High quality sequence stop: 722. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Toshiyuki and Piero Carninol (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
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602689093F1 NIH_MGC_97 Homo sapiens cDNA
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Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Nucle: this is a NIH_MGC Library." a 295 c 263 g 143 t
                                                                                                  /clone_lib="NIH_MGC_97"
//lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag ): Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched
                                                                                for full-length clones and constructed using the
                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:4821598"
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Brownstein (NHGRI), Shiraki
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Query Match Best Local Similarity

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                                                           Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                               1 (bases 1 to 712)
NIH-MGC http://mgc.nci.nih.gov.
National Institutes of Health,
Unpublished (1999)
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          CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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Plate: LLAM10402 row
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/lab_host="DH10B (phage-resistant)"
/note="organ: bladder; vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally; oligo-dT prim
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technolog
Note: this is a NIH_MGC Library."

a 221 c 211 g 163 t
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/clone="IMAGE:4514200"
/clone_lib="NIH_MGC_93"
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Tissue Procurement: ATCC/DCTD/DTP
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1 (bases 1 to 838)

NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin: Vector: pOTB7: Site_1: XhoI: Site_2: EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
90 a 306 c 282 g 158 t 2 others
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/clone_lib="NIH_MGC_20"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                   Plate: LLCM1837 row: 1 column: High quality sequence stop: 783.
                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 801)
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602861314F1 NIH_MGC_17
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                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{DNA}} Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoFSite_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using following 5' adaptor: GGCACGAG(G). Size-selected
                                                                                                   /clone="IMAGE:5020563"
/clone_lib="NIH_MGC_17"
                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                    /organism="Homo sapiens"
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                                                                     Mus musculus
discovery
                      Bonaldo, M.F.,
                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                 to 664)
            and
                      Lennon, G. and Soares, M.B
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87.9%;
           subtraction:
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Rodentia;
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Pred. No. 1.4e
0; Mismatches
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                                           Craniata; Ver
Sciurognathi;
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97044477
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Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   considered under appropriate and limited collaborative arrangements Seq primer: M13 Forward
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Tel: 301 443 1706
Fax: 301 443 9890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.

TAG_SEQ-None found"

1 238 c 207 g 142 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="U1-M-CG0p-beu-e-08-0-UI"
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/lab_host="DH10B_(Life_Technologies)"
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Pred. No. 4.5e-65;
0; Mismatches 87;
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Room 7N-7190, J
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420

GCTGATGGTTGTCACTGGCATCCTCCTGGCCTATGTGGCAGGCTGGGTCCTANAGTGGCG

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JOURNAL COMMENT
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AUTHORS
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GCCCGAGACCCCACGTTTTCTCCTCACTCAACACCAGTACCAGGAGGCCATGGCTGCCTT
                                                                                                                                   516;
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Plate: LLAM10672 row: c column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 677)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
Unpublished (1999)
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BG707107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Location/Qualifiers
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                                                                                                                                   Conservative
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                                                                                                                                                                                                                                       /note="Organ: brain: Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sali-XhoI (gtcgag); Oligo-dT primed using primer 5 TTTTTTTTTTTTTTTTTTTTTTVTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 254 c 241 g 122 t
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_96"
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Pred. No. 5.5e-65;
0; Mismatches 1;
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                                                                                                                                                                                                                                                    Unpublished (***)
Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                                                                                                                                            9712 Medical Center Dr.,
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                       Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., , I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                     146
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79
                                                                                     a
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGD"
/note="Vector: pBluescriptSKm"
185 c 169 g 151 t
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Score 477; DB 10;
Pred. No. 3.8e-64;
0; Mismatches 11
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1307 ttctgtgtccctgaaactaaaggaaagactctggaacaaatcacagcccattttgagggg

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3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

Search completed: February 13, 2002, 13:37:33 Job time: 2980 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_ba:*
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Gapop 10.0 , Gapext 1.0
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gb_ov:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	UL 76 ES ES ES		NO. SC 1 75 2 74 4 48 6 38 7 48 7 32 7 5 6 38 7 32 7 32 7 32 10 26 11 26 10 10 11 12 11 12 11 12 11 10 11 10 11 10 12 26 13 12 13 12 14 11 15 10 16 10 17 10 18 10 19 27 19 27 27 22 28 27 29 27 20 28 21 28 22 28 23 33 24 33 25 27 27 33 28 36 29 37 30 38 31 37 32 38 33 39 36 34 40 66 44 66 45 66	, L
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Matches Query Match Best Local

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GLUTXI, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
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CTVPPVTGFAVITAARDVWMLLGGRLLTGLACCVPPTLMLLLMCYMPETPRFLLTQHQYQEA
MAALRFLWGSEEGWEEPPVGAEHOGFOLAMLRRPGVHKPIGICLMVFQQLSGVNAI
MFYANTIFEEAKFKDSSLASVTYGILVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGB
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Ishibashi, K.
Molecular cloning of a new pupulished Only in DataBase ("hases 1 to 2189)
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AB033418.1 GI:7592743
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Rattus norvegicus
Rattus norvegicus
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Submitted (08-OCT-1999) to the DDBJ/EMBL/GenBank databases. Kenichi Ishibashi, Jichi Medical School, Pharmacology; Minami-kawachi, Kawachi, Tochigi 339-0498, Japan (E-mail:kishiba@jichi.ac.jp, Tel:81-285-87326, Fax.81-285-44-5541)
Location/Qualifiers
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Sequence 5
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                                                                                                                                         Glutx polypeptide family and nucleic acids encoding Patent: WO 0104145-A 5 18-JAN-2001; University of Lausanne (CH)
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1 (bases 1 to 2072)
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AUTHORS
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AJ245936
AJ245936.1 G1:701860
glucose transporter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem.
20138191
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Ibberson, M., Uldry, M.
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Mammalia; Eutheria; Rodentia;
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a novel mammalian glucose transporter expressed
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PWLLMSSIFPLHVKGVATIGICUJNWEMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL
SVLFTLTVVPETKGRTLEQVTAHFEGR"

673 c 584 g 464 t
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/db_xref="taxon:10090"
21. .1454
                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                  /gene="GLUTX1"
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nsporter; GLUTX1
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Rodentia;
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AUTHORS

Carayannopoulos, M.O., Chi, M.M., McKnight, R.A., Mueckler, M., Deva

Devaskar,S.U.

Cui,Y.,

Pingsterhaus,J U. and Moley,K.

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GYSSPA.IPSLRETAPPALRLGUNAASWFGAVVTLGAAAGGILGGWLLDRSGRKLSLLL
CTVPFVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAPVISEIAYPAVRGLLGSV
VQLMVVTGILLAYVAGWVLEWRWLAVLGCVPFTLMLLLMCYMPETPRFLLTQHOYQEA
MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
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SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGIIVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="glucose transporter GLUT8"
/protein_id="AAF78366.1"
/db_xref="GI:8671758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.4%;
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Pred. No. 1.3e-76;
0; Mismatches 72;
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                                                          ctcatgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtgtcctc
                                                                                                                                                                       accaactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctc
                                         CTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGTGTGGCTACCGGCATCTGTGTCCTC
                                                                                                         GGCAGCATGTGCCTCTTCATTGCTGGCTTTGCGGTGGGGCTGGGGACCCATCCCCTGGCTC
                                                                                                                        ggcagcatgtgcctcttcatcgctggttttgcagtaggctgggggacccatcccctggctc 174
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REFERENCE
AUTHORS
TITLE
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                                                       Query Match
Best Local Sim
Matches 351;
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tcaccagattctgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doege,H., Schurmann,A., Bahrenberg,G., Brauers,A. and Joost,H.G. GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxicology, Technical University Aachen, Wendlingweg
Aachen, FRG
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Y17802
                                                                          Similarity
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                                                                                                                                                                         222
                                                         Conservative
                                                                                                                                                                       a
                                                                                                                                                                                                                                                           /codon_start=1
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CULMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHGYQEA
WAALRFLWGSEEGGWEEDPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
                                                                                                                                                                                        SVLFTLTVVPETKGRTLEQVTAHFEGR"
                                                                                                                                                                                                        SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
                                                                                                                                                                                                                                              MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="GLUT8"
26. .1459
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="GLUT8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
26. .1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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87.8%;
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Rodentia;
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                                                                        Score 321.6; DB 1
Pred. No. 8.5e-62;
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                                                                                          DB 10;
                                                         49;
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                                                                                          Length 1490;
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DEFINITION ACCESSION
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Best Local S
Matches 311
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     228
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                                                  ctggctcctcatgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctg 227
                                                                                                                gacggtgacggaccctttctgtgactggcagccctgagc 454
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tgtcctcaccaactggttcatggcctttctggtgaccaaagagtttaacagcatcatgga
                                   GTGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCCACCGGCGTCTG
                                                                                                 GGCGGTGGGCAACATGTGCCTCTTCATCGCCGGCTTCGCTGTGGGCTGGGGGGCCCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACCCTACGGTGCCTTCTGGCTCACCGCTGCCTTCTGCGCTCTCAGTGTCCTATTCACA 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (13-NOV-2000) Anatomy and Cell E
Medicine, Martin Luther University Halle,
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Augustin,R., Navarrete-Santos,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halle 061097, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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AF321324
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                                                                                                                                                                                                                                                                                                                                                                      /product="glucose transporter 8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
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<1. .1012
                                                                                                                                                                                                                                                                                                                                                    MAFLVTKEFSSLMEVLRPYGAFWLASAFCIFGVLFTLACVPETKGKTLEQITAHFEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Glut8"
<1. .1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Glut8"
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                                                                                                                                                                                                                                           26.5%;
83.6%;
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                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                              Score 274.4; DB 4;
Pred. No. 2.9e-51;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                           302 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anatomy and Cell Biology,
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                                                                                                                                                                                                                                                           Length 1012;
                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Faculty of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001
                                                                                                                                                                                                                              0;
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GGCGCCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGGCTGGCCTGGCCTGGCCGTGGG 1153 ggtgcccatctccgcagagcctgctgatgttcacctggggctggcctggcctggctgtagg 116

57

Matches

305;

Conservative

Similarity

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
20283667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucose transporter 8; GLUT8 gene. human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-1998) H. Joost, Toxicology, Technical University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Homo sapiens mRNA
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(bases 1 to 1508)
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                                                                                                                                                                   /gene="GLUT8"
/gene="GLUT8"
/codon_start=1
/codon_start=1
/product="glucose transporter 8"
/product="glucose transporter 8"
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translation="MPPEDPESTQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFAL/
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GYSSPA PSLQRAADVMMLLGGRLTGLACGVASIJVAPVYISEIAYPAVRGLLGSC
VQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTOHRRQEA
MAALRFLWGSEDGWEDPPIGAEDSFHLALLRQPGIYRFFIIGVSLMAFQQLSGVNAVM
                                                                                          PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF SVLFTFSCVPETKGKTLEQITAHFEGR" a 519 c 477 g 318 t
                                                                                                                                         FYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTS
AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                                                              /gene="GLUT8"
27. .1460
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27. .1460
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Score 272.6; DB 9; Pred. No. 7.8e-51; D; Mismatches 54;
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Aachen, Wendlingweg 2, D~52057
                             DB 9;
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                                  1353 GCCCTATGGAGCCTTCTGGCTTGCCTCCGCTTTCTGCATCTTCAGTGTCCTTTTCACTTT
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                                                    accctacggcgccttctggctcaccgctgccttctgtatcctcagcgtccttttcacgct
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Sequence
AX179740
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1 (bases 1 to 2080)

Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Reddy, R.,
Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Yao, M.G.,
Gandhi, A.R., Tang, Y.T. and Khan, F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transporters and ion channels Patent: WO 0146258-A 28 28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Eukaryota; M
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/db_xref="taxon:96101"
/note="Incyte ID No: 1416107CB1"
/note="Incyte ID No: 1416107CB1"
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Pred. No. 1.8e-50;
0; Mismatches 55;
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                           CAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAG
                                                                                                                                                 cagcatgtgcctcttcatcgctggttttgcagtaggctggggacccatcccctggctcct 176
                                                                               CAACATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTCGGGGCCCCATCCCCTGGCTCCT
accctacggcgccttctggctcaccgctgccttctgtatcctcagcgtccttttcacgct
                                        caactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctcag
                                                                                            catgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtgtcctcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUTX1, a novel mammalian glucose transporter central nervous system and insulin-sensitive t J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                           Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose transporter; GLUTX1 gene
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AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGNMCLFIAGFAVGWGPI
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/codon_start=1
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Best Local :
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   1655
                                                                                                                                                                                                                                                                                  1415 GGCGCCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGGCTGGCCTGGCCTGGCCGTGGG 1474
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                                                                                                                                                                                                                            117 cagcatgtgcctcttcatcgctggttttgcagtaggctgggggacccatcccctggctcct 176
                                 297 accetaeggegeettetggeteaeegetgeettetgtateeteagegteetttteaeget 356
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GCCCTATGGAGCCTTCTGGCTTGCCCTCCGCTTTCTGCATCTTCAGTGTCCTTTTCAGTTTT
                                                                                      caactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctcag
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                                                                                                                                                                                                                                                                                                    cacctttgtccctgagactaaaggcaggactctggaacaaatcacagccca-tttgaggg 415
                                                                    CAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAG
                                                                                                                                        CATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGCATCTGCGTCCTCAC
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/db_xref="G1:12711199"
/translation="MrpEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFAL
/translation="MrpEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFAL
GYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVLFTLFCVPEIKGKTLEQITAHFEGR"
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PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
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FYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTS
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VQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted CB10 1SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECTOR: pBACe 1.6 the entire insert of clone RP11-356B19 The This sequence is the entire insert of clone RP11-373JB is at 96439 in this sequence. Tright end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/Chr9
RP11-356B19 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Apr 26, 2001 this sequence version replaced gi:13277497. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
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                                                                                                                                                        /clone="RP11-356B19"
/clone_lib="RPC1-11.2"
23455._23821
/note="Single clone region. Assembly confirmed
restriction_digest_data."
/note-"Single clone region. Sequence from reads from short insert library derived from a single pUC clone. Restriction digest data confirm the assembly." 225123. .225370
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/chromosome="9"
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Mammalia; Eutheria;
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PGGVRGALGATPOLMAVFGSLSLYALGLLLPWRWLAVAGGGPVLYMIILLSEWPNSPR
FLLSKSRDEFALQALIMLRADSEVHWEFEQIDDUNRROSSRVSWABAMERPYVFRILI
TVLMRFLQQLTGITPILVYLQTIFDSTSVVLPSQQDAAIVGAVRLLSVILAAVTMDLA
GRKVLLYVSASIMFVANLTLGLYVQLVPRTLTPNSTVEIVTLGGTEQPPAAAFNYLTIL
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TPLLATMLFIMGYAMGWGPITWLLMSEVLPLARAGVASGLCYLVSWLTAFVLTKYFLL
                                                                                      AVNAFGLQVPFFFFSAICLLSLLFTGCCVPETRGRSLEQIEÄFFHTRRMSFRP* 621 c 593 g 459 t 1 others
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                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product"
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Sciurognathi; Muridae; Murinae;
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CCCGAGACCAAGGGACGGTCCCTGGAGCAGATC
                 cctgagactaaaggcaggactctggaacaaatc
                                                           CCTTTCTTCTTCGCGGCCATCTGCTTGGTGAGCCTGGTGTTCACAGGCTGCTGTGTG 270
                                                                             gccttctggctcaccgctgccttctgtatcctcagcgtcctttttcacgctcacctttgtc
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1 (bases 1 to 378)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genes and gene expression products Patent: WO 0102568-A 2890 11-JAN-2001;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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AAF55866
                                                                                                                                                                                                      Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                           14-JUL-1999; 99US-0143907.
27-AUG-1999; 99US-0151140.
23-FEB-2000; 2000US-0184285.
13-JUL-2000; 2000US-0616132.
         P-PSDB; AAB66933
                   WPI; 2001-112615/12.
                                      Thorens B,
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                                                                                                                                               18-JAN-2001.
                                                                                                                                                                                     Rattus sp.
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Query Match Best Local Sin Matches 756;

Similarity 75... 56; Conservative

46.68;

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for murine GLUTX1

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperqlycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence

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27 - AUG - 1999;
23 - FEB - 2000;
13 - JUL - 2000;
                                                                                                Claim
                                                                                                          Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disorce.g. is chemia and diabetes -
                                                                                                                                                                              Thorens
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Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemot lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter and ion channel-1; TRICH-1; vaccine; cystic
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fibrosis;

stroke;

sapiens

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Location/Qualifiers 46..1479 /*tag= a
/*rag= a
/product= "Human TRICH-1 protein"
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WO200146258-A2

22-DEC-2000;

2000WO-US35095

23-DEC-1999; 99US-0172000

14-JAN-2000; 21-JAN-2000; 28-JAN-2000; 02-FEB-2000; 10-FEB -2000; 2000US-0176083. 2000US-0177332. 2000US-0178572. 2000US-0179758. 2000US-0181625.

(INCY-) INCYTE GENOMICS

Baughn ". Khan MR, Burford Azimzai FA; , Y, Au-Young Yue H, J, Lu Nguyen DAM, Yang J, Yao MG, J, Reddy Gandhi R, AR; Lal P;

P-PSDB; 2001-418042/44 DB; AAE04888.

and Novel human preventing transporter and ion channel ing transport, neurological, muscle proteins ns useful for treating and immunological

Claim 5; Page 140-141; 160pp; English.

disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arrhritis, scleroderma, Sjogren's disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, ammesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's The present sequence is transporter and ion channel 1 (TRICH-1) cDNA TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, systemic lupus erythematosus Wilson's disease, cataracts, and other diseases including pulmonary

RESULT AAD09552 ID AAD

w

AAD09552

standard;

cDNA;

artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholasterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic

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RESULT
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27-AUG-1999;
23-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GLUTX1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2001
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      acids encoding
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84.7%;
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No. 8.2e-49;
transporter proteins,
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Best Local :
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                                                                                                             1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTXI.
1775 gcgatgacagccactcattaggggatgg
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                     acggtgacggacccctttctgtgactgg
                                                                cacctttgtccctgagactaaaggcaggactctggaacaaatcacagccca-tttgaggg
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                                                                                                                     accotacggcgccttctggctcaccgctgccttctgtatcctcagcgtccttttcacgct 356
                                                                                                                                                        caactggctcatggcctttctcgtgaccaaggagttcagcagcctcatggaggtcctcag
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                                                                                                                                                                                                                                                                                                                                   320;
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82.5%;
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                                                                                                                                                                                                                                                                                                                                                                            Score 268.8;
Pred. No. 2.5e
0; Mismatches
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nes 67;
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AAA44914/c
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  cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; Huntington's disease; coagulation disorder; parkinson's disease; Huntington's disease; coagulation disorder;
                                                                                                                            immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostat thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antivicer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                         expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAA44914 standard;
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                                                                                                                                                                                                                                                                                                                                                                           AAA44914;
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                                                                                                                                                                                                                mouse; chicken; rat; secreted expressed sequence tag; sE
sed sequence tag; EST; probe; chemotactic; proliferative;
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                    expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
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ID NO:1489

haemostatic; antifungal;

SEST;

inflammatory

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Matches 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or vital infections, depression and observed the stroke of the stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment autoimmune disorders antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsroilatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease), tumours, bacterial, fungal or viral infections, psoriasis. AAA45926 to AAA45931 represent linker variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
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ccaaagagtttaacagcatcatggagatcctcagaccctacggcgcc 309
                                                                                         TCAAGGGCGTGGCGACAGGCATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCTCGTGA
                                                                                                                                  | Caaggglgtggctaccggcgtctgtgtcctcaccaactggttcatggcctttctggtga
                                                                                                                                                                                                                                                               TTGCGGTGGGGCTGGGGCCCATCCCCTGGCTCCATGTCAGAGATCTTCCCTCTGCATG
                                                                                                                                                                                                                                                                                                   ttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttccctctgcaca
                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGGAGCCCAGCCCTGCGGACCCTGATGCCTGTCTTGCCTGTCTCGCTCCCACAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579 BP; 109 A; 184 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to AAA45925 represent specifically claimed secreted expressed tags (sESTs), isolated from human, mouse, chicken and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treacy M,
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64.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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Pred. No. 7e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for rat GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia hypoglycaemia; glucose metabolism disorder; neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                            acageettegteeteaetaagtaetteetgetggeagtgaatgeetteggeeteeaggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding
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2000US-0184285.
2000US-0616132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to GLUTX proteins (AAF55865-AAF55871 and 366941). The GLUTX proteins are related to the facultative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ibberson
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Pred. No. 1e-1
0; Mismatches
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cc polynucleotides. The library is used to detect differentially expressed cc genes correlated with a cancerous state of a mammalian cell and can cc detect colon, prostate, breast and lung cancer. The library can be used cc to produce probes for detection of mRNA and to produce additional copies cc the polynucleotides. The probes can be used for chromosome mapping of cc the polynucleotide and for detection of transcription levels. Ribozymes cr antisense oligonucleotides can be generated. The polynucleotides and cc their gene products are used as genetic or biochemical markers (e.g. in carcinogenesis pathway and/or monitor the earliest changes along the cc carcinogenesis pathway and/or monitor the efficacy of therapies and cc preventive interventions. The polynucleotides, polypeptides and cc treat the cancers and proliferative disorders such as neoplasia, xx
                     Qy
                                           Query Match
Best Local Sim
Matches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams LT, Esc
Reinhard C, Rand
Crkenjakov R, DJ
Kita D, Garcia V
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 974; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                        Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                     127
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1444
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF67134;
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                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367
ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag
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cancer; lung
                                                                                                         378
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Randazzo F,
R, Drmanac S,
rcia V, Jones
                                                                                                         BP;
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99US-0142311.
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                                                      10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; cancer detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                  Innis MA, Garcia PD,
Kennedy GC, Pot D, L
Dickson M, Labat I,
LW, Strache-Crain B;
                                         Score 109.8;
Pred. No. 1.3e
0; Mismatches
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                                      Gaps
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RESULT
AAA23461
ID AAA2
XX AAA2
XX AAA2
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XX Huma
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24-AUG-1998;
09-SEP-1998;
28-SEP-1998;
28-SEP-1998;
23-DEC-1998;
23-DEC-1998;
                                                                                                                       Claim
                                                                                                                                                                      diseases
                                                                                                                                                                                                                   New secreted
                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                        Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hood disorder; haemophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma: contracention;
                                                                                                                                                                                                                                                                                                                                                                                     (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1999;
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DB; AAY95019.
                                                                                                                     86; Page 335; 357pp;
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                                                                                                                                                                                                                                                                                                                                      D,
                                                                                                                                                                                   or transmembrane proteins and polynucleotides encoding for treating neurodegenerative disorders, autoimmune
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98US-0109978.
98US-0113645.
98US-0113646.
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                                                                                                                  English
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                                                                                                                                                                                                                                                                                                                                 наll J,
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The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A32462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the

transmembrane proteins.

The proteins of the

and

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RESULT
AAC80569
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Best Local
                                                                                                    Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing; nervous system disorder; aging; chemotaxis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regime. Diseases or conditions that may be treated using the proteins of nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, asthma and anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              additionally be useful as contraceptives. Nucleic acid sequences of invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents cDNA encoding one of the 40 proteins of the invention.
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WO200058467-A1
                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC80569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC80569 standard; cDNA; 1577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccines,
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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62.6%;
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0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAR45119 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1577 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alternative polypeptides encoded by the genes, and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -  \frac{1}{2} \sum_{i=1}^{n} \frac{1}{2} \sum_{i=1}^{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the isolation and characterisation
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cccgagaccaagggacggtccctggagcagatc
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                                                                                                                                                      cctttcttcttcttcgcggccatctgcttggtgagcctggtgttcacaggctgctgttgtg
                                                                                                                                                                                               gccttctggctcaccgctgccttctgtatcctcagcgtcctttttcacgctcacctttgtc
                                                                                                                                                                                                                                                                                                         accgccttcgtcctcaccaagtccttcctgccagtggtgagcaccttcggcctccaggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 A; 496 C;
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Pred. No. 1.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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AAF55870 standard;

cDNA; 1541 BP

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Query Match
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                  1400
                                                                                                                                                                 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66937-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose bindling and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTX3.
                                                                                                                                                                                                                                                1280
                                                                                                                                                                                                                                                                                                                               1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1541 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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2000US-0616132.
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Дb

treatment of Parkinson's disease, disease), to modulate activin and fertility), to modulate chemotact

to modulate activin and

Huntington's disease and Alzheimer's inhibin activity (e.g. for controlli

for controlling

chemokinetic

polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate

rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the

may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynuclectides and its complementary sequences may also be used as DNI probes in diagnostic assays and also used in gene therapy. The

DNA

The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides

Claim

Page 287-289;

563pp; English.

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RESULT 11
AAD12574
                                                                                                                                                                                                  Human proteins with hydrophobic domains them, useful for preventing diagnosing a Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                            03-FEB-2000;
03-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntington's disease; Alzheimer's disease; chemotactic; chemo haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                 Kato
                                                                                                                                                                                                                                                                                                                                               06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
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SAGAMI CHE
                                                                                                                                                                                                                                                                 Kimura
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; 2000JP-0000588.
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                                                                                                                                                                                                                                                                                                                                                                                                                   "CDS is specifically is claimed in claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth activity; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disorder; antimicrobial;
                                                                                                                                                                                                          s and the nucleic acids encoding and treating e.g. cancer,
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RESULT 1
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Best Local Similarity 73.0
Matches 119; Conservative
25-FBB-1999
05-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1461 BP; 195 A; 501 C; 456 G; 309 T; 0 other;
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Similarity 55.9%;
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99US-0125788

99US-0126785

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                                                                                                                                                                                                                              Arabidopsis thaliana
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Pred. No. 2.4e-07;
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99US-0131449.
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protein identification; signal transduction pathway;
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                                                                                           pathway; promoter;
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nilarity 55.9%;
Conservative (
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                  2000EP-0301439
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Pred. No. 2.4e
0; Mismatches
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2.4e-07;
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PRIOR APPLICATION UNMBER: US 5,405,941
FILING DATE: 15-Apr-1995

PRIOR APPLICATION DATA: US 5,405,941
FILING DATE: 15-Apr-1993
PRIOR APPLICATION NUMBER: 08/323,460
FILING DATE: 14-Oct-1994
PRIOR APPLICATION OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr. Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/440,421
FILING DATE: 15-May-1995
PRIOR APPLICATION UNMBER: 08/354,516
FILING DATE: 21-FEB-1995
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TITLE OF INVENTION: METHOD
TITLE OF INVENTION: RESPONS
NUMBER OF SEQUENCES: 12
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SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: 1
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ADDRESSEE: Lahive and Cockfield
                                                                PRIOR APPLICATION DATA:
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                               APPLICATION NUMBER: PCT/
FILING DATE: 14-OCT-1994
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                                                                                                                                                                              APPLICATION NUMBER: 08/354,516
FILING DATE: 21-FEB-1995
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/472,934 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER:
                                                                                                APPLICATION NUMBER:
                                                                                                                                 APPLICATION NUMBER: US 5,405,941 FILING DATE: 15-Apr-1993
                                                                                                                                                                                                                                      FILING DATE:
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                                                                                   FILING DATE:
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nes 90; Conserv
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                                               PCT/US94/11690
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PCT/US94/04178
                                                                                              08/323,460
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Pred. No. 9.8e-06;
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Best Local .
TELEFAX: 3
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LIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/323 ***
CLASSIFFTO: 14-CCm-22
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                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                         FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/049,254
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TITLE OF INVENTION:
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NAME: Giulio A. DeConti, Jr. Esq.
NAME: 31,503
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          TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
                                                                REGISTRATION NUMBER:
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                                                                                NAME:
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Local Similarity 66.2%;
nes 90; Conservation
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Pred. No. 9.8e-06;
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Best Local Similarity
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                                                                                                                                                                   FILING DATE: 15-APK-1222
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/323,460
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APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
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LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-APR-
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Lahive and Cockfield
TELECOMMUNICATION INFORMATION:
                                                       ATTORNEY/AGENT INFORMATION:
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               REFERENCE/DOCKET NUMBER:
                          NAME: KARA, Catherine REGISTRATION NUMBER: P
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                                                                          15-APR-1994
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05-JUN-1995
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14-OCT-1994
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             CPI-004CN3
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Pred. No. 9.8e-06;
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Best Local S
Matches 90
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TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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              FILING DATE:
                                                         APPLICATION NUMBER: FILING DATE: 14-OCT
                                                                                                         FILING DATE:
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                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER: US 08/354,516
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les 90; Conserv
                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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            15-APR-1994
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                                                         14-OCT-1994
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                                                                                                                      US 08/323,460
                            PCT/US94/0417E
                                                                                                                                                                  US 08/049,254
                                                                         PCT/US94/11690
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Pred. No. 9.
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9.8e-06;
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                                                          PRIOR APPLICATION DATA:
                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL MEKK PROTEINS NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                     APPLICATION NUMBER: PCT/I
FILING DATE: 14-OCT-1994
                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 5-JUNICLASSIFICATION: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: P41,100
REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                               FILING DATE:
                                             APPLICATION NUMBER:
                                                                                                                                                            APPLICATION NUMBER: US 08/049,254 FILING DATE: 11-APR-1993
                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 GGCTTCCTTTTCATCG 138
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nes 90; Conserv
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STRANDEDNESS: double
TOPOLOGY: linear
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LOCATION: 466
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                                                                                                                                                                                                                        NUMBER: US/08/461,145C
5-JUNE-1995
                              15-APR-1994
                                                                                                                    UMBER: US 08/323,460
14-OCT-1994
                                                                                                                                                                                                                                                                                                             Floppy disk
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66.2%;
US 08/354,516
                                         PCT/US94/04178
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Best Local 9
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                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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              PRIOR APPLICATION DATA:
                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                               PRIOR APPLICATION DATA:
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LENGTH: 2503 base pairs
TYPE: nucleic acid
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                    APPLICATION NUMBER: US 0 FILING DATE: 14-OCT-1994
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  APPLICATION NUMBER:
                                                                                                                                                          CLASSIFICATION:
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPI-
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90; Conservative
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N: 530
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                                        PCT/US94/11690
                                                                                 US 08/323,460
PCT/US94/04178
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Best Local :
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REFERENCE/DOCKET NUMBER: CPI-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                     APPLICATION NUMBER: 08/931
FILING DATE: SEPTEMBER 17,
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ISOFLAVONE BIOSYNTHETIC ENZYMES NUMBER OF SEQUENCES: 9
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                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
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                            REGISTRATION NUMBER:
                                                                                                                  CLASSIFICATION:
                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                         19898
                                                                                                                                                                                                                                                                                                 WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kara, Catherine J
                                                                                                                                                                                                                                                                                     DELAWARE
                                                                                                                                                                                                                                                                                                              E: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                           FADER, GARY MICHAEL
                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                    08/931,668
BER 17, 1997
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                                                                                                                                                US/09/154,874
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              BB-1098-A
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Pred. No. 9.8e~06;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
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US-08-300-903A-8
US-08-300-903A-8; Sequence 8, Application US/08300903A
· Patent No. 5591630
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                     TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO:
                        SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M
APPLICANT: Giri, Judith G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000
                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple OF
                                                        TELEPHONE: 205 June 109 TELEPHONE: 205-233-0644
                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1223 base pairs TYPE: nucleic acid STRANDEDNESS: single
             TYPE:
                                                                                                                           NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 06-SE
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER:
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STRANDEDNESS:
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          nucleic acid
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55..1223
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55..990
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                                                                                                                                                                                                                                              NUMBER: US/08/300,903A
06-SEPTEMBER-1994
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Query Match
Best Local Similarity
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                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,9
FILING DATE: 03-JANUARY-1996
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 21-JUNE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                NAME: Hanson, No. 584056
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/644,116 FILING DATE: 10-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
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                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Felfe & Lynch
805 Third Avenue
                                                                                                            2085 base pairs
                                                                                                                                                       (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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3..839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.5 inch, 360 kb storage
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                                                                                                                                                                                                                          No. 5840568man D.
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85.0%;
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96.9%;
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 Score
Pred.
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 60.8; DB 2;
No. 2.2e-05;
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             Length 2085;
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Db Qy Db

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US-08-905-445-7
; Sequence 7, A
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 07-JUNE-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 04-AUG-1CASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 03-JAN
                                                                                                                                       STRANDEDNESS:
                                                                                                                                                     TYPE:
                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                NAME: Hanson, No. 5864015man REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/66 FILING DATE: 21-JUNE-1996
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                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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1 tggcggccgctctagaactagtggatcccccgggctgcaggaattcggcacgagctggtg 60
                                        62;
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New York City
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                                                                                                                                                  nucleic acid
                                                                                                                                                                                                           (212) 838-3884
                                        Conservative
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                                                                                                                           linear
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                                                                                                                                                                                                                           (212) 688-9200
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                                    Score 60.8; DB z;
Pred. No. 2.2e-05;
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                                                                 Length 2085;
                                       Indels
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                                     0;
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                                                                                                                                                                             RESULT 13
US-09-071-224-3
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                                                                                                                                             Sequence 3, Application US/09071224
Patent No. 6271343
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 69; Conserv
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                                                                                                                               GENERAL INFORMATION:
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                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            1000 aaaaaaaaaaaaaaaaaaaaaaa 1023
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                               APPLICANT: Lok, Si
APPLICANT: Presnell,
                                                                                                                                                                                                                                              2544 AAAAAAAAAAAAAAAAAAAAAA 2567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2567 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bienkowski, Michael J.
TITLE OF INVENTION: No. 6031089el Sequences of p56, a Proteins Which
TITLE OF INVENTION: Affects K-ATP Channels
                  APPLICANT:
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wootton, Thomas A REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 301 Hen: CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/993,260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pharmacia and Opjohn, Co., Intel. Prop. Law ADDRESSEE: (1920-32-LAW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
.NT: Jelmberg, Anna C.
.NT: Gilbert, Teresa
.NT: Foster, Donald C.
.NT: Adams, Robyn L.
.NT: Lehner, Joyce M.
.FINVENTION: MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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82.1%;
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Pred. No. 3.6e-05;
0; Mismatches 15
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; LOCATION: 88...13 ; OTHER INFORMATION: US-09-071-224-3
                                                                                                                                                                                                                                                         US-08-722-126A-4
                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                     Sequence 4, Application US/08722126A
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                                                                                                                                                       APPLICANT: PECHT, Israel APPLICANT: GUTHMANN, Mar APPLICANT: TAL, Michael
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ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                          TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA) NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                       1725 AAAAAAAAAA 1735
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LENGTH: 1813 base pairs
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 206-442-6678
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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STREET: 1:
             COUNTRY:
                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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20004
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             UNITED STATES
                                                                                                                                                                      GUTHMANN, Marcelo D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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90.1%;
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             OF AMERICA
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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PCT-US95-04258-4
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Best Local Similarity
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                           STREET: 419 Sever CITY: Washington STATE: D.C.
                             APPLICATION NUMBER: PCT/US95/04258 FILING DATE: 06-APR-1995
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BROWDY, ROGER L.
REFERENCE/DOCKET NUMBER: PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
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                                                                                                          Matches
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Best Local Similarity
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
               1012 aaaaaaaaaaa 1023
|||||||||||||||
1429 AAAAAAAAAAAA 1440
                                                   FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION.UMBER: 25,618
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                        64;
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54..617
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                                                                                                      Score 59.2; DB 5;
Pred. No. 4.6e-05;
0; Mismatches 8
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Search completed: February 13, 2002, 13:34:39 Job time: 2806 sec

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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## ALIGNMENTS

RESULT

REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE BI275901/c LOCUS COMMENT DEFINITION ACCESSION JOURNAL MEDLINE ORGANISM Email: msoarss@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565 bi2/5901 563 bp. mRNA EST 19-JUL-2001 UI-R-CXO-bxh-h-03-0-UI.S1 UI-R-CXO Rattus norvegicus cDNA clone UI-R-CXO-bxh-h-03-0-UI 3', mRNA sequence. Genome Res. 6 (9), 791-806 (1996) 97044477 1 (bases 1 to 563) Bonaldo, M.F., Lenno Normalization and s Contact: Soares, MB Eukaryota; Metazoa;
Mammalia; Eutheria; Rattus BI275901.1 GI:14920290 Seq primer: M13 Forward discovery Rattus. norvegicus Lennon,G. and Soares,M.B. and subtraction: two approaches to Chordata; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; facilitate gene IA 52242, USA

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RESULT
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                                                                         TAGCCAGCTTACCCATCACTTACAGGTTCTCTCCAACTCTTCCCTGGTCTCAGTGTCCTG
                                                                                                                            TTGTCTTGTCAACCAAGTCCTTTTCAGAGTGCCCAGAGACCTCCGGATTCACCTTGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=rat placenta pool TAG_SEQ=TCACGACAGT" 141 c 163 g 124 t
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TAG_LIB=UI-R-CX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CX0 library is a normalized library constructed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Organism="Rattus norvegicus"
/Strain="Sprague-Dawley"
/db_xref="taxon:10116"
/Clone="UI-R-CXO.bxh-h-03-0-UI"
/Clone_lib="UI-R-CXO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="ADULT"
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                      acaaatcacageccatttgagggacggtgacggacccctttctgtgactggcagccctga
                                                                                                                                           taacagcatcatggagatcctcagaccctacggcgccttctggctcaccgctgccttctg 332
                                                                        TATTCTTAGCGGCCTTTTCACGCTCACCTTTGTCCCTTTGGACTAAAGGCAGGACTTTGGA
                                                                                           tatcotcagcgtcctttttcacgctcacctttgtccctgagactaaaggcaggactctgga 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induced by peripheral nerve axotomy Unpublished (2001)
Contact: Zhang xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P
Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiao,H.S., Han,Z.G., Zhang,F.X., Huang,Q.H., Lu,Y.J., Bao,L., Fr
,Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G., Chen,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG672321 538 bp mRNA LSI DRNCFD10 Rat DRG Library Rattus norvegicus cDNA clone DRNCFD10 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG672321.1 GI:13894420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
146 c 138 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="dorsal root ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Rat DRG Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DRNCFD10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ∕organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         35.1%;
86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                    Score 364; DB 11;
Pred. No. 2.7e-40;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 g
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat dorsal root ganglion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccacaccatgagettcaccagattctgaggetentgnagectgetgcacacacaggacat 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCGGAGGCATG 491
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BF420038.1
EST.
                                                                                                                                                                                                                                                                                                                                                                      The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tay present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF420038 450 bp mRNA EST UI-R-BJ2-bpm-c-04-0-UI.Sl UI-R-BJ2 Rattus norvegicus UI-R-BJ2-bpm-c-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 450)
Bonaldo, M.F., Lennor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                       primer: M13
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            /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the followin tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 11.5 dpc, Ventricle at 15 dpc, Ventricle at 15 dpc, Ventricle at 15 dpc, Ventricle at 15 dpc, NV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="spraque-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bpm-c-04-0-UI"
                                                                                                                                                                                                               /clone_lib="UI-R-BJ2"
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                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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Rodentia;
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                993
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                                                                                                                                                                                                                                                              Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A., Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D., Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \rm H34451 319 bp mRNA EST 13-M EST111406 Rat PC-12 cells, NGF-treated (9 days) Rattus end similar to Glucose transporter, mRNA sequence.
                                                                                                                      Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                         The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                             Contact: Lee, NH
                                                                                                                                                                                                                 95396786
                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H34451.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H3445
                                                Email: nhiee@tigr.org
For clone availability please
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                               factor treatment
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TAG_SEQ=ACAAC"
105 c 117
                                 Location/Qualifiers
/organism="Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:979868
                    . 319
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96.7%;
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Pred. No. 6.9e-34;
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                                                                                       contact
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13-MAR-1998

sp. cDNA 5'

Murinae;

Database

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the
                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iow
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317;
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On Jun 5, 1998 this
                                                                                                                                                                                                                                                discovery
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                        Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                    UI-R-CO-hq-f-01-0-UI.S1 UI-R-CO Rattus norvegicus UI-R-CO-hq-f-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                  Rattus.
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                                                                                                  Eckstein Medical Research Building Iowa City, 319 335 8250 319 335 9565
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/db_xref="taxon:10118"
/db_xref="taxon:10118"
/clone_lib="mat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript SK:; Site_1: EcoRI; Site_2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
and directionally cloned using the Lambda ZAP II Vector
Kit by Stratagene"
80 9 88 t 1 others
                                                                                                                                                                                                                                                                                                                                             Metazoa;
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; Rodentia;
                                                                                                                                                                                             sequence version replaced
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Pred. No. 8.4e-34;
"'Amatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                       Muridae;
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ID=1773689
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               118
                                                                                                                                                         //deb/bost="MPHIOB (Life Technologies)"
//deb/bost="MPHIOB (Life Technologies)"
//ore="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I, Site_2: Eco RI; The UI-R-CO library is a subtracted library derived from the UI-R-Al and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTS had been derived was used as a driver in a hybridization with single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH1OB barreria (Life Technologies) to generate the UI-R-CO
           മ
                                               bacteria (Life Technologies) to generate the UI-R-CO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="UI-R-c0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-C0-hq-f-01-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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993 aaaaaa 998 9 TCACTTACAGGTTCTCTCCAGCTCTTCCCTGGTCTCAGTGTCCTGGATCATTAGTCACCA agtcetteteagagtg-ecaaagaceteeggatteacettggggttageeggttaececa tcacttacaggttctctccaactctcagctggtctcagtgtcctcggatcattagtcacca tcagaaacaaggtcaggtgagtccaggaagaaagagaatggttcttgtcttgtcaacca tgcgggctcctggctctagtgctctggctgggcatcttttggggtgcttggtcctaagcaa 693 ctgcccatacctcacttgactgggggatgagaaagggacttagccacataagatttgggc 753 AGTCCTTCTCAGAGTGCCCAGAGACCTCCGGATTCACCTTGGGGTTAGCCAGCTTACCCA CTGCCCATACCTCACTTGACTGGGGGATGAGAAAGGGACTTAGCCACATAAGATTTGGGC 354; Similarity Conservative 30.4%; 96.7%; 0; Score 315.6; DB 10; Pred. No. 9.1e-34; Mismatches 9; Indels Length ω •• Gaps 7 992 66 126 813 186 245

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TITLE
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                                                                                           accaactggttcatggcctttctggttgaccaaagagtttaacagcatcatggagatcctc 294
                                                                                                                                               CTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGTGTGGCTACCGGCATCTGTGTCCTC
                                                                                                                                                                  ctcatgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtgtcctc
                                                                                                                                                                                                                       GGCAGCATGTGCCTCTTCATTGCTGGCCTTGGCGGTGGGGCTGGGGACCCCATCCCCTGGCTC
                                                                                                                                                                                                                                        ggcagcatgtgcctcttcatcgctggttttgcagtaggctgggggacccatcccctggctc 174
                                                                                                                                                                                                                                                                                               AGACCCTACGGTGCCTTCTGGCTCACCGCTGTCTTCTGGCTCTCAGTGTCCTATTGCCAC
                                                                         ACCAACTGGTTCATGGCCTTTCTAGTGACCAAAGAGTTCAGCAGCGTCATGGAGATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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BF120840
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601757442F1 NCI_CGAP_Mam5 Mu
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National Institutes of Health, M
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Plate: LLAM9192 row: d column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:3986651"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57/B6"
/db_xref="taxon:10090"
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76.5%;
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Pred. No. 2.1e-33;
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Matches Query Match Best Local

304;

Conservative

Similarity

26.1%; 84.7%;

Score 271; DB Pred. No. 6.9e 0; Mismatches

DB 11; 5.9e-28; 1es 55;

Length 949; Indels

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 949)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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BG749509.1
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602707648F1 NIH_MGC_43 Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                      160
                                        California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
                                                                                                   /clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming Directionally cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
                  (Stratagene) and Superscript II
Note: this is a NIH_MGC Library.
302 c 264 g 223 t
                                                                                                                                                                                                                                                                                /clone="IMAGE:4844411"
                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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   al Similarity 82.
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                                                                                                                                                                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
Plate: 70 row: A column: 21
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed wi
v0.980904.e. Vector identified by cross_match with the
                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 546)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                76
                                                                                                ۵
                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                         /note="Vector: pCMV SPORT6; Site_1: XbaI; Si
Library made from pooled tissue from day 11,
and 30 embryos."
182 c 162 g 124 t 2 others
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                 25.9%;
    0,
                Score 268.2; DB 10;
Pred. No. 2e-27;
 Mismatches
 Indels
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Sus.
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Laegreid, W.W.
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                                                                M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21,
                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized ventricle at 16.5 dpc library cDNA Library Preparation:
                                     >AT_rich#Low_complexity
Seq primer: M13 Forward
                                                                                                                                                                                                                                                        Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                     University of Iowa
451 Eckstein Medical Research Building Iowa
                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF420257 295 bp mRNA EST UI-R-BJ2-bpk-g-03-0-UI.Sl UI-R-BJ2 Rattus norvegicus UI-R-BJ2-bpk-g-03-0-UI 3', mRNA sequence.
BF420257
                                                                                                                                                                                                                                                                                                                         Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                         discovery
                                                                                                                                                                                                                                                                                                                                                                                                                    Normalization and subtraction: two
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, M.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 295)
                                primer: M13
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Lennon, G. and Soares, M.B.
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source

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF551290 426 bp
UI-R-CO-hq-f-01-0-UI.
UI-R-CO-hq-f-01-0-UI
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
                                                             Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                 1 (bases 1 to 426)
Bonaldo, M.F., Lenno:
                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
                                                                                                                                                                            Contact: Soares, MB
                                                                                                                                                                                                  97044477
                                                                                                                                                                                                                   Genome
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                                                                                                                                                                                                                 Res. 6 (9),
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/clone_lib="UI-R-BJ2"
/clone_lib="UI-R-BJ2"
/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies) with a modified note="Wector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the followin tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 15 dpc, ventricle at 16.5 dpc, av canal at 15 dpc. For a detailed description of the library from which this clone was derived, please the library from which this clone was derived, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon MSoares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                               Metazoa;
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63 c 6
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                                                                                                                                                                                                                                                                                   Lennon, G. and
                                                                                                                                                                                                                   791-806
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Pred. No. 1.3e-24;
Pred. No. 1.3e-24;
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                                                                                                                                                                                                                                                           approaches
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VERSION KEYWORDS

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                                                                                                                                                                                                                                          cctaagcaactgcccatacctcacttgactgggggatgagaaagggacttagccacataa
                         tgtcaaccaagtccttctcagagtg-ccaaagacctccggattcaccttggggttagcca
                                                                                                                TGACGAGACTGCGGGCTCCTAGTCGCTCTAGTGCTCTGGCCAGGCATCTTTGGGGTGCTTGGT
TGTCAACCAAGTCCTTCTCAGAGTGCCCAGAGACCTCCGGATTCACCTTGGGGTTAGCCA
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//lab_host="build" (Life Technologies)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to
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/dev_stage="adult"
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/db_xref="taxon:10116"
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TITLE
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cacctttgtccctgagactaaaggcaggactctggaacaaatcacagcccatttgaggga 416
                                                    accctaeggcgccttctggctcaecgctgccttctgtatcctcagcgtccttttcacgct
                                GCCCTATGGAGCCTTCTGGCTTGCCTC-CCTTTCTGCATCTTCAGTGGTCCTTTTTCACT
                                                                                                              caactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctcag
                                                                                                                                                                         catglcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtgtcctcac
                                                                                                                                                                                                                   CAGCATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGGGGGGCCCATCCCCTGGCTCCT
                                                                                           CAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAG
                                                                                                                                                         CATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGCATCTGCGTCCTCAC
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Plate: LLAM9706 row: i column:
High quality sequence stop: 710.
                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE910478 934 bp mRNP
601501005F1 NIH_MGC_70 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 934)
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BE910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_70"
/tissue_type="epithelioid carcinoma"
/tas_host="DHIOB (phage=resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
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291 c
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/db_xref="taxon:9606"
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TITLE
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Best Local
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tctgtatcctcagcgtccttttcacgctcacctttgtccctgagactaaaggcaggactc 388
                                    GTTCAGCAGCCTCTATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGCTTGCCTCCGCTT
                                                      gtttaacagcatc-atggagatcctcagaccctacggcgccttctggctcaccgctgcct 328
                                                                                                                      tgtggctaccggcgtctgtgtcctcaccaactggttcatggcctttctggtgaccaaaga 269
                                                                                                                                                                       GGGCTGGGGGCCCATCCCTGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGG
                                                                                                                                                                                       aggctggggacccatcccctggctcctcatgtccagagatcttccctctgcacatcaaggg 209
                                                                                                                                                                                                                                         CGTGGGGCTGGCCTGGCCGTGGGCAGCATGTGCCTCTTCATCGCCGG-CTTGCGGT
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                                                                                                                                                                                                                                                                                                             292;
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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1 (bases 1 to 712)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:4514200"
/clone_lib="NIH_MGC_93"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DHHOB (phage-resistant)"
/note="forgan: bladder; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
                                                                                                                                                                                                                                                                                                                                                                                                        full-length clones and constructed by Note: this is a NIH_MGC Library." 221 c 211 g 163 t
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Sutheria; Primates; Catarrhini;
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Pred. No. 1.6e-22;
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Best Local Similarity
Matches 298; Conserv
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                                                                                                                                                                                     tttggggtgcttggtcctaagcaac-tgcccatacctc-acttgactgggggatgagaa- 726
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                                                                                                                                                                     TTTGGGGTGCTTGGACCTAAGCAACTTGCCCATACCTCNACTTGACTGGGGGGATGANAAA 255
agggacttagccacataagatttgggctcagaaacaaggtcaggtgagtccaggaagaaa 786
                                                                                                           AGGGACTTAGCCACATAAGATTTGGGCTCAGAAACAAGGTCAGGTGAGTCCAGGAAGAAA
                                              AGAGAAT-GTTCTTGTCTTGTCAACCAAGTCCTTCTCAGAGTGCCCAGAGACCTCCGGAT 136
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., RA., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Lee,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability please contact
(tdbinfo@tdb.tigr.org)
Seq primer: Ml3 - 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute for Genomic Research 2, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (301)-838-3529
(301)-838-0208
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nhiee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT principle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus sp."
/db_xref="ATCC (inhost):2005377"
/db_xref="raxon:10118"
/clone="RPNBT28"
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
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74 c 79 g
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95.5%;
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Rodentia;
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Sciurognathi;
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                                                                                                                                                                                                                                                               Length 324
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ZAP II Vector
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KEYWORDS
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AL565390/c
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Best Local 9
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CCNCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGT
                cctcaccaactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagat 290
                                                                                    tcctcatgtcagagatctt--ccctctgcacatcaagggtgtgggctaccggcgtctgtgt 230
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                                                                  TCCTCATGTCAGAGATCTTCCCCCCTCGCACTNTCAAGGGCGTGGCGACAGGCATCTGCGT 552
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                                                                                                                                                                                                                                                                             290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prime, mRNA sequence. AL565390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL565390 752 bp mRNA EST 16-FEB-2001 AL565390 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSODF005YE02
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                                                                                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Fetal brain; Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                              http://fulllength.invitrogen.com"
206 c 242 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            week, 24 week and 26 week)"

/lab_host="DH10B"

/note="Grace"
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/dev_stage="pooled tissue fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CSODF005YE02"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                         Score 218.6; DB 10;
Pred. No. 8.4e-21;
2; Mismatches 67;
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AZ985752/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: 0 column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2m0267011R mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2m0267011 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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              polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWn942 (gi14732114/gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical
                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0267011"
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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Rodentia;
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Search completed: February 13, Job time: 2987 sec 2002, 13:37:40

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

source	FEATURES	TITLE JOURNAL	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX076669	RESIII.T 1
12087 /organism="Rattus sp."	University of Lausanne (CH) Location/Qualifiers	Glutx polypeptide family and nucleic acids encoding same Patent: WO 0104145-A 3 18-JAN-2001;	Thorens, B., Ibberson, M. and Uldry, M.	1 (bases 1 to 2087)	Rattus.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Rattus sp.	Rattus sp.		AX076669.1 GI:12711200	AX076669	Sequence 3 from Patent WO0104145.	AX076669 2087 bp DNA PAT 06-FEB-2001		

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                                                                        Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne, CH-1005, SWITZERLAND
                                                                                                                                                                                Ibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammalian glucose transporter expressed
central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                 Direct Submission
                                                                                                                                                 Ibberson, M.R.
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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//translation="MSPEDPOGETQPLLRSPGARAPGGRRVELATFAAALGPLSFGFAL
//translation="MSPEDPOGETQPLLRSPGARAPGGVLGGWLLDRAGRKLSLLL
GYSSPAIPSLERTTAPPALRLGDTAASWFGAVVTLGAAAGGVLGGWLLDRAGRKLSLLL
GYVPTGFAVITAARDVWMLLGGRLLTGLACGVASLVARVYISEIRYPAVGLLGSC
VQLMVVTGIILAYVAGWVLEWRWLAVLGCVPFTLMLLLMYMPETPRFLLTOHOVQEA
MAALRFLWGSZEGWWEBPPVGAEHQGFOLAMTRRPGVHKPLIIGICLMVFQQLSGVWAI
MFYANTIFEBAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRKLLALAGGVIMYFSM
SAFGTYFKLTQSGPSMSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGP
IPWLLMSEIFPLHKKVAATGVCVLTINWFMAFLVTKEFNSIMEILRPYGAFWLTAAFCII
SAFGTYFKLTQSGPSMSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGP
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                                                    Direct Submission
Submitted (08-0CT-1999) to the DDBJ/EMBL/GenBank databases. Kei Ishibashi, Jichi Medical School, Pharmacology; Minami kawachi, Kawachi, Tochigi 329-0498, Japan (E-mail:kishiba@jichi.ac.jp, Tel:81-285-58-7326, Fax:81-285-44-5541)
                                                                                                                                                                                                                                                AB033418.1 GI:7592743
AB033418.1 GI:7592743
glucose transporter 8.
Rattus norvegicus cDNA to mRNA, clone_lib:testis.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Wammalia: Eutheria; Rodentia; Sciurognathi; Muric
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Ishibashi, K.
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/db_xref="taxon:10116"
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/product="glucose_transporter"
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VQLMVYTGIILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTGQQYQEA
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MFYANTIFEEAKFKDSSLASVTYGIIQVLFTAVAALIMDRAGRKLLLALSGVINVFSM
SAFGTYFKLTQSGPSNSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGP
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30. .1466
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Pred. No. 1.2e-59;
; Mismatches 0;
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Sequence
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Mus sp.
Eukaryota; Metazoa; Chordata; Crania
Bukaryota; Butheria; Rodentia; Sciuro
1 (bases 1 to 2072)
Thorens,B., Ibberson,M. and Uldry,M.
                                                                                                                                                                  Glutx polypeptide family and nucleic Patent: WO 0104145-A 5 18-JAN-2001;
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CVQLMVVTGILLAYVACWVLEWRWLAVLGCVPPTLMLLLMCYNFPTFLTTOHOYQE
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109. .1548
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109. .1548
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                                                                                                                                   Location/Qualifiers
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Pred. No. 1.2e-59;
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Sciurognathi;
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                                                                                                                                                                                                          Submitted (02-SEP-1999) Ibberson M.R., and Toxicology, University of Lausanne CH-1005, SWITZERLAND
                                                                                                                                                                                                                                                                                                                             GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                             Direct Submission
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1 673 c 584 g 464 t
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                                                                                                                                                        /organism="Mus musculus"
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J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                                                                                                                                                                              Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057
                                                                                                                                                                                                                                                                Direct Submission
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MAALRFLWGSEEGWEEDPVGAHHQGFQLALLRRPGIYKPLIIGISLMVPQQLSGVNAI

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                                                                                                                                                                                       Submitted (07-FEB-2000) OB/Gyn, Ave, St. Louis, MO 63110, USA
                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                      Moley, K.H., Carayannopoulos, M.O. and Cui, Y
                                                                                                                                                                                                                                                                                                                                         Carayannopoulos,M.O., Chi,M.M., Cui,Y., Pingsterhaus,J.M., McKnight,R.A., Mueckler,M., Devaskar,S.U. and Moley,K.H.
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                      49.
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                                                                                                                      /strain="129"
                                                                                                                                                                       Location/Qualifiers
                                                                                                    /db_xref="taxon:10090"
                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:7688220"
                                                                                                                                                         .1843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucose
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                                                                                                                                                                                                       Washington University, 4566 Scott
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.6e-49;
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Best Local
                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tttctggtgaccaaagagtttaacagcatcatggagatcctcagaccctacggcgccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCTGCATGTCAAGGGTGTGGCTACCGGCATCTGTGTCCTCACCAACTGGTTCATGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGCTGGCTTTGCGGTGGGGCTGGGGACCCATCCCCTGGCTCCTCATGTCAGAGATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttc
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Bos taurus glucose t
AF321324
AF321324.1 GI:14582
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Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COW
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Augustin,R.,
                                                                                                                                                                                                                                                                                                                                                  Halle
                                                                                                                                                                                                                                                                                                                                                                         Medicine,
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                                                                                                                                                                                                                                                                                                                                                ine, Martin Luther University Halle, 061097, Germany
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LFTATAAALIMDRAGRRLLLTLSGVVMVFSTSAFGTYFKLTEGGPSNSSHVDLPALVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mspedpoetopllrppeartprgrrvflasfaaalgplsfgfal
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<1. .1012
                                                                                                                                                                                                 /gene="Glut8"
<1. .1005
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                                                                                                                                                                             /gene="Glut8"
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           .1012
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91.1%;
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1.6e-49;
hes 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                    and Fischer, B.
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RESULT AF321324

8

FEATURES

gene

MAALRFLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVM

REFERENCE

AUTHORS TITLE

JOURNAL

SOURCE KEYWORDS VERSION ACCESSION DЬ δÃ В Qy Вþ QУ В QΥ Вb

181

1312

241

οy

1132

61

1192

QY DЬ Qy Вþ QΥ Вр Q

Db Qy ДĎ

121

Matches

ORIGIN

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MEDLINE
REFERENCE
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TITLE
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TITLE
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hes 243;
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                                                                                                                                                                                                                                                                                                                                                                                     Doege,H., Schurmann,A., Bahrenberg,G., Brauer GLUT8, a novel member of the sugar transport with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                                                                                                                                                                                                                                   Submitted (16-JUL-1998) H. Joost, Institution of the Toxicology, Technical University Aachen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA
Y17801
                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                           Aachen,
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                                                                                                                                                                                                                                                          Location/Qualifiers
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86.5%;
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Pred. No. 2.3e-44;
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litator family
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Best Local Similarity
Matches 242; Conserv
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Best Local :
                                           1190
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ctctgcacatcaagggtgtggctaccggcgtctgtgtcctcaccaactggttcatggcct
                                TCGCCGGCTTTGCGGTGGGGCTGGGGCCCATCCCCTGGCTCCTCATGTCAGAGATCTTCC
                                                tcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttcc 121
                                                                                          AGCCTGTTGATGCCAGCGTGGGGTGGCCTGGCTGGCCGTGGGCAGCATGTGCCTCTTCA 1189
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2080)
Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B.
Gandhi, A.R., Tang, Y.T. and Khan, F.A.
Transporters and ion channels
Patent: WO 0146258-A 28 28-JUN-2001;
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AX179740
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Location/Qualifiers
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                                                                                                                                                                                                                                                   /Organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 1416107CB1"
688 c 632 g 460 t
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AFGAYFKLTQGGFONSSHVAISAPVSAQPVDASYGLAWLAVGSWCLFIAGFAVGWGPI
PWLLMSELFPLHVKGVAFGICTULTUNLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
SVLFTFSCVPETKGKTLEQITAHFEGR"
a 519 c 477 g 318 t
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                                                                                                                                                                              77.7%;
86.4%;
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86.4%;
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Pred. No. 3.9e-44;
0; Mismatches 38
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JOURNAL
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TITLE
                                                                                                                    1088 AGCCTGTTGATGCCAGCGTGGGGCTGGCCTGGCTGGCCGTGGGCAACATGTGCCTCTTCA 1147
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122 ctctgcacatcaagggtgtggctaccggcgtctgtgtcctcaccaactggttcatggcct 181
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                                                                62 tegetggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttcc 121
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                                                                                                                                           2 agoctgotgatgttcacctggggctggcctggctggctgtaggcagcatgtggcctcttca 61
                                         TOGECOGETTTGCGGTGGGGTGGGGGCCCATCCCCTGGCTCCTCATGTCAGAGATCTTCC 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammallian glucose transporter expressed in the central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH-1005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1873) Tibberson,M., Uldry,M., and Thorens,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ibberson, M.R.
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AJ245937
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     /translation="MTPEDPEETOPLIGPPGGSAPRGRRVFLAAFAAALGPLGFGFAL
GYSSPAIPSLQRAAPPAPRLDDAAASWFGAVTLGAAAGGVLGGWLVDRAGRKLSLLL
CSVPFVAGFAVITAAQDVWMLLGGRLLFGLACGVASIVAPVTLSEIAXYPAYRGLLGSC
VQLMVVGILLAYLAGWVLEWRRLAVLGCVPPSLMLLMCFMPETPRFLLTQHRRQEA
MAALRFLWGSEQGWEDPPIGAEQSFHLALLRQFGIYKFFIIGYSLMAFQQLGGVVAW
FYAETIFEEAKFKDSSLASVVGGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTS
AFGAYFKLTQGGFGNSSHVAISAPVAGDFUDASVGLAWLAVGHWCLFIAGFAYGWGFI
PWLLMSEIFFLHVKGVATGICVLTNMLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
EWLLMSEIFFLHVKGVATGICVLTNMLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
SVLFTLFCVPEIKGKTLEQITAHFEGR"

621 c 573 g 400 t
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/product="gutosse transporter"
/protein_id="CAB75702.1"
/db_xref="GI:7018366"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="GLUTX1"
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86.1%;
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for glucose transporter (GLUTX1 gene).
                                                                                                                                                                                                           0,
                                                                                                                                                                                                       Score 217.6; DB 9
Pred. No. 9.6e-44;
0; Mismatches 39
                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                          Length 1873;
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DEFINITION ACCESSION
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Best Local S
Matches 241
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ggctcaccgctgccttctgtatcctcagcgtccttttcac 281
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                                                                                           ctctgcacatcaagggtgtggctaccggcgtctgtgtcctcaccaactggttcatggcct 181
                                                                                                                                                                                                                                           tcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttcc 121
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                   ggctcaccgctgccttctgtatcctcagcgtccttttcac 281
                                                                                                                                                CTCTGCATGTCAAGGGCGTGGCGACAGGCATCTGCGTCCTCACCAACTGGCCTCATGGCCT
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                                                                        TTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCT 1671
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Location/Qualifiers
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Thorens,B., Ibberson,M. and Uldry,M
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SVLFTLFCVPEIKGKTLEQITAHFEGR"
3 750 c 672 g 475 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAC28495.1"
/db_xref="G1:12711199"
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/db_xref="G1:12711199"
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CSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGGC
VQLMVVVGILLAVLAGGVLEWRRLAVLGCVPPSLMLLLMCFWPETPRFLLTQHRRQEA
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/db_xref="taxon:9606"
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FYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTS
AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGNMCLFIAGFAVGWGPI
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86.1%;
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Pred. No. 9.5e-44;
0; Mismatches 39;
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/clone_lib="RPCI-11.2"
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/chromosome="9"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SMISSPROT; Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on Apr 26, 2001 this sequence version replaced gi:13277497. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-356B19 The left end of clone RP11-373J8 is at 96439 in this sequence. Tright end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                   /note="Single clone region. Assembly confirmed restriction digest data." 65019. 65283
/note="Single clone region. Sequence from reads short insert library derived from a single pUC Restriction digest data confirm the assembly." 57092 c 57267 g 54682 t
                                                                                                                                                         short insert library derived from a Restriction digest data confirm the 225123. .225370
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                                                                                                                                                                                                                                                                                                     ACCGCCTTCGTCCTCACCAAGTCCTTCCTGCCAGTGGTGAGCACCTTCGGCCTCCAGGTG
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Sequence
AX072418
Homo sapiens mRNA (SLC2A6 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Reinhard, C., Crkenjakov, R., Drmanac, S., Dickson, M., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Grebberg, G., Crkenjakov, R., Drmanac, S., Crkenjakov, R., Drmanac, S., Drandac, S., Drmanac, S., Drmana
                                                          HSA17803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genes and gene expression products Patent: WO 0102568-A 2890 11-JAN-2001; CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Pred. No. 4.9e-12;
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                              transporter
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MEDLINE
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                                                                                                                                                                                                                                                    1256 CTCTTCATCATGGGCTACGCCGTGGGCTGGGGTCCCATCACCTGGCTGCTCATGTCTGAG
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                                                                                                                                                                                          | 115 atcttccctctgcacatcaagggtgtggctaccggcgtctgtgtgtcctcaccaactggttc
                                                                                                                                                                                                                                                                                                                                     Local Sinhes 141;
                                                                                                                                                                                                                                                                         55 ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag
CCTTTCTTCTTCGCGGCCATCTGCTTGGTGAGCCTGGTGTTCAC
                   gccttctggctcaccgctgccttctgtatcctcagcgtccttttcac
                                                                                 ACCGCCTTCGTCCTCACCAAGTCCTTCCTGCCAGTGGTGAGCACCTTCGGCCTCCAGGTG
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Y17803.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose transporter 6,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                     Similarity 62.
11; Conservative
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RELLSRGRDEEALRALAWLRGTDVDVHWEFEQIQDNVRRQSSRVSWAEARAPHVCRPI
TVALLMELLQOLFGITPILVYLQSIFOSTAVLLÞFKDDAAIVGAVRLLSVLIAALTMD
LAGRKVLLFVSAAIMFAANLTLGLYIHFGPRÞLSPNSTAGLESESWGDLAQPLAAPAG
YLTLVÞLLATMLFIMGYAVGWGPITWLLMSEVLÞLRARGVASGLCVLASWLTAFVLTK
SFLÞVVSTFGLQVÞFFFFAAICLVSLVFTGCCVÞETKGRSLEQIESFFRMGRRSFLR"
a 552 c 492 g 320 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="facilitataive glucose transporter g (GLUT6)"
/protein_id="CAB96996.1"
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47. .1570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mQepllGaeGpDyDTfpEKpppSpGDRARVGTLQNKRVfLATfA
AVLGNfSfGYALVYTSPVIPALERSLDPDLHLTKSQASWFGSVfTLGAAAGGLSAMIL
NDLLGRKLSIMFSAVPSAAGYALMAGAHGLWMLLLGRTLTGFAGGLTAACIPVYVSEI
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62.1%;
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Pred. No. 4.3e
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Search completed: February 13, Job time: 8093 sec

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1: /SIDS2/gcgdat
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Gapop 10.0 , Gapext 1.0
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/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen
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## ALIGNMENTS

AAF55866

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AAF55866 standard; cDNA; 2087

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17-APR-2001

(first entry)

disease

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14-JUL-1999; 27-AUG-1999; 23-FEB-2000; 13-JUL-2000; P-PSDB; AAB66933 Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disea WPI; 2001-112615/12 Thorens B, Ibberson M, 14-JUL-2000; 2000WO-IB01042 18-JAN-2001. WO200104145-A2 Rattus Rat GLUTX1 coding sequence. ф UNIV LAUSANNE. ; 99US-0143907. ; 99US-0151140. ; 2000US-0184285. ; 2000US-0616132. Uldry M;

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                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; shypoglycaemia; glucose metabolism disorder; neurodegenerative dis
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                                                     (UYLA-) UNIV LAUSANNE
                                                                                                        13-JUL-2000;
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Pred No. 2.5e-72;
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                                                                                                       Sequence 2072 BP; 351 A; 673 C;
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Local Similarity
nes 257; Conser
                                                                                                                                                                                                                                                                                                                                                                                                          prevention,
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91.5%;
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Mismatches
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10-SEP-2001

(first entry)

transporter and ion channel-1 (TRICH-1) cDNA.

demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; malabsorption transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis;

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Best Local Similarity
Matches 242; Conserv
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14-JAN-2000; 2000US-0176083.
21-JAN-2000; 2000US-01777332.
28-JAN-2000; 2000US-0178572.
02-FEB-2000; 2000US-0179758.
10-FEB-2000; 2000US-0181625.
                                                                                                                                                                                                                                                                               including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
                                              1190
                                                                                                        1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                       purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and Parkinson's disease, demyelinating diseases, mental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 140-141; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAE04888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS
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                 122
                                                                          62
                                                                                                                                    Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is transporter and ion channel-1 (TRICH-1) cDNA is used as vaccine. TRICH is useful for treating a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing transport,
                                                                                                                   ctctgcacatcaagggtgtggctaccggcgtctgtgtcctcaccaactggttcatggcct 181
                                                         tcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttcc 121
                                                                                                   tcgccggctttgcggtgggctggggcccatccccttggctcctcatgtcagagatcttcc
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                                                                                                                                                                                                                                         2080
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Azimzai Y,
                                                                                                                                                                Conservative
BP;
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Yue H,
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Nguyen
                                                                                                                                                             No. 4.2e-54;
smatches 38;
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Yao MG,
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                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTX1.
        1432
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                                                                                                                                                                                                                                                                                                                                                                Sequence 2217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2000;
13-JUL-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the prevention,
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                                                                                                                                                                   241;
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                                                                                                                                                                                                     Similarity
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99US-0151140
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86.1%;
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Pred. No. 1.3e
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AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antinflammatory; cytostatic; antipacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiuicer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene
                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                     Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                   WPI; 2000-317938/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunomodulatory, haematopoietic; chemokinnetic; analgesic; haemostatic thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; resulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; central nervous system disorder; Alzheimer; disease; stroke; Parkinson; disease; Huntington s disease; cagulation disorder; haemophilia; thrombosis; inflammatory disease; Crohn's disease; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                     Merberg D,
                                                                                                                                                                                                                                                                                                                                    Jacobs K,
                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200021991-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
expressed sequence tag; EST; probe; chemotactic; proliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted expressed sequence tag SEQ ID NO:1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2000
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                                                                                                                                                                                                                                                                                                                McCoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           98US-0104436
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                                                                                                                                                                                                                                                                                                                             LaVallie
                                                                                                                                                                                                                                                                                                              Bowman
                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                              e ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis; ss.
                                                                                                                                                                                                                                                                                                                        Collins-Racie
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and rat
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antifungal;
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ACCOMMENS OF STREET STR
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AAF67134
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Best Local S
Matches 148
                                                                                            Williams LT, Escobedo J, Reinhard C, Randazzo F, Crkenjakov R, Drmanac S,
                                    WPI; 2001-091805/10
                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                  02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                                                                                                                                            W0200102568-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, parkinson's, Huntington's disease, stroke), coagulation disease), tumours, bacterial, fungal or viral infections, depression and in the exemplification of the present linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 ttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctcagaccctac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
cancer; lun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148;
                                                                                Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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99US-0142311.
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                                                                                Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
g cancer; cancer
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                                                                    , Innis MA, Garcia I
Kennedy GC, Pot D,
, Dickson M, Labat :
S LW, Strache-Crain ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer detection;
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Pred. No. 5.2e-27;
0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer; prostate
er detection; ss.
                                                                    Garcia PD,
Pot D, I
Labat I,
1e-Crain B;
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n, Lamson
resh
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                                                                                                        Klinger J,
amson G, Drm
                                                                                          Leshkowitiz
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                                                                                     C J, Kassam
Drmanac R;
itiz D;
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Library of polynucleotides for diagnosing

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the
                24-AUG-1999;
                                                   02-MAR-2000
                                                                                                                                                                                                                                           blood disorder; haemophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                 cDNA encoding human secreted protein vql_1, SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA23461 standard; cDNA; 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes correlated with a cancerous state of a mammalian cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                              Human; secreted protein; cancer; tumour; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 974; 1046pp; English
                                                                                  WO200011015-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accgccttcgtcctcaccaagtccttcctgccagtggtgagcaccttcggcctccaggtg 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperplasia.
                99WO-US19351
                                                                                                                                                    Location/Qualifiers 54..371
                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ence is one of 3351 sequences in a library of human The library is used to detect differentially expressed
                                                                                                                                      /*tag=
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                                                                                                                     "Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.4; DB 22;
Pred. No. 1.1e-16;
"" ematches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
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                                                                                                                   protein vq1_1"
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Best Local
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24 - AUG-1998;
09 - SEP-1998;
28 - SEP-1998;
25 - NOV-1998;
23 - DEC-1998;
23 - DEC-1998;
23 - AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following: cytokine activity; cell proliferation; differentiation; immune
                                                                                                                                                                                                                                                                                                                                                                                                                         additionally be useful as contraceptives. Nucleic ac invention may be used in chromosome mapping, and as diagnostic primers and probes. The present sequence encoding one of the 40 proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins nucleotides of the invention include autoimmune diseases: genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and thrombolytic activity; anti-inflammatory activity; and tumour inhibition activity. The proteins may be administered to patients as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 86; Page 335; 357pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valenzuela D,
                                                                         177
 237
                                    235
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                                                                                                                                                                                                                                         ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag 114
cetttettettegeggeeatetgettggtgageetggtgtteae
                                 gccttctggctcaccgctgccttctgtatcctcagcgtccttttcac
                                                                                                                                                                 atcttccctctgcacatcaagggtgtggctaccggcgtctgtgtgtcctcaccaactggttc 174
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                                                                     accgccttcgtcctcaccaagtccttcctgccagtggtgagcaccttcggcctccaggtg
                                                                                                      atggcctttctggtgaccaaagagtttaacagcatcatggagatcctcagaccctacggc 234
                                                                                                                                             gtcctgccctgcgtgcccgtggcgtggcctcagggctctgcgtgctggccagctggctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                                                                                                                                                                                                                                 141;
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY95019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                            823
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                            В₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or transmembrane proteins and polynucleotides encoding for treating neurodegenerative disorders, autoimmune % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0097638.
98US-0097659.
98US-0099618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yuan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0113645
98US-0113646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0379246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0109978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0102092
                                                                                                                                                                                                                                                                                                                                                                                          170 A;
                                                                                                                                                                                                                                                                                                                31.7%;
                                                                                                                                                                                                                                                                                                                                                                                            257 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                           Score 89.4; DB Z1,
Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                          233 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall J,
                                                                                                                                                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                                                                                            T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rapiejko
                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a source of
                                    281
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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or

0

AAC80569 ID AAC8

AAC80569 standard; cDNA; 1577

ВP

Human secreted protein gene

39

SEQ ID NO:49

12-FEB-2001

(first entry)

antiproliferative;

secreted

protein;

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Qy
                                                             Query Match
Best Local :
                                              Matches
                                                                                                                                       Sequence 1577
                                                                                                                                                                                       tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-080530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of the capabilities.
                                                                                                                                                                                                                                                       bacteria, viruses and fungi and ocular disorders e.g. corneal infection or the polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary
                                                                                                                                                                                                                                                                                                                                         e.g. rheumatoid arthritis, nyperprovince describes e.g. cardiac arrest, of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebral ischaemia, anglogenesis, nervous cerebrovascular disorders e.g. cerebral ischaemia, anglogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                           fungicide; and opthalmalogical. The secreted proteins, polynucleotides antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of their activities include immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive, antientation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent alternative polypeptides encoded by the genes, and amino acid sequence
                                                                                                                                                                                                                                                                                                                                     system disorders e.g. Alzheimer's disease, infections caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 371-372; 440pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; neuroprotective; opthalmalogical; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200058467-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system disorder;
           55
ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-611712/58
                                                            Similarity
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben
                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US07505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0126502.
99US-0172410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; immunosuppressive; antiarthritic; antirheumatic; e; cytostatic; cardiant; vasotropic; cerebroprotective; protective; antibacterial; virucide; fungicide; cancer; autoimmune disease; hyperproliferative disorder; autoimmune disease; hyperproliferative disorder;
                                                                                                                                     352 A; 496
                                                          31.7%;
62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aging;
                                        Score 89.4; I
Pred. No. 1.9e
0; Mismatches
                                            0,
                                                                                                                                     Ç;
                                                                                                                                     445
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                                                                                                                                   G;
                                                                                                                                   284
                                    DB 21;
1.9e-16;
hes 86;
                                                                                                                                 T; 0
                                                                                                                                                                                      of the genes
                                                                                                                                 other;
                                        Indels
                                                                         Length
                                      0
                                                                                                                                                                                      proteins
                                                                                                                                                                                                                                                                                                                     infection
                                      Gaps
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Qγ

55 ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag 114

Query Match Best Local Similarity 62.1

31.7%;

Score 89.4; DB Pred. No. 2e-16;

459 T; 1 other;

0;

Mismatches

66; 22;

Indels Length

Gaps

0;

2011; 0;

Sequence

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RESULT
AAAF55871
ID AAFE
XX AAFE
XX AAFE
XX AAFE
XX Rat;
DT 17-/
XX Rat;
XX Rat;
XX Rat;
XX Hexc
KW hypc
OS Ratt
XX NO2(
XX Rat;
PD 18-(
XX I4-,
PR 27-)
PR 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                                             The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a percent of the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorder: e.g. ischemia and diabetes -
                                                                                   neurodegenerative for rat GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 82-83; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB66938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-2000; 2000WO-IB01042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; GLUTX; gene therapy; vaccine; hey
hexose transport disorder; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat GLUTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF55871 standard; cDNA; 2011 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471
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        2011 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
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2000US-0184285
2000US-0616132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucose metabolism disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0143907
    337 A; 621 C;
                                                                                                                        disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                The present sequence
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593 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hexose transport modulator;
ia; diabetes; hyperglycaemia; ss;
disorder; neurodegenerative disease.
                                                                                                                        is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                coding
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                                                   Matches
                                                                                                                                                                                               AAB66912-AAB66941). The GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the codino carriers for human GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
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                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disorders to the prevention of the contract of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thorens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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ctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagag 114
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)B; AAB66937.
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                                                   Conservative
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2000US-0616132
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                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n, diagnosis and treatment and diabetes -
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99US-0151140
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                                                                                                                                                                  209
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61.7%;
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                                                DB 22;
5.4e-16;
hes 87;
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                                                Indels
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                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                        cells they are expressed in, such as: antiinflammatory; antirheumat antiarthritic; immunosuppressive; antibacterial; endocrine; cardian central nervous system; virucide; anti-HIV; fungicide; antimutagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1220
                                                                         AAM25963. The proteins can have activities based on i
                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1340
                                                                                                                             Claim 1; Page 564; 1217pp; English.
                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                 (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
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                                                                                                                                                            isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                 HYSEQ INC
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2000US-0488725.
2000US-0552317.
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                                                                                              human proteins
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                                                                                on the tissues
                                                              antirheumatic;
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                                               cardiant;
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cardiovascular;

antianaemic; antiaggregant; haemostatic;

vulnerary;

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RESULT 12
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Best Local Similarity 66.5
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                                                                                      Claim 2; Page 34-35; 60pp; English.
                                                                                                                                                                       New hexose carrier proteins used to manipulate carbohydrate transport
                                                                                                                                                                                                                                      WPI; 1999-620438/53
P-PSDB; AAY49625.
                                                                                                                                                                                                                                                                                                                          Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexose carrier protein; corn; rice; sorghum; soybean; wheat; carbohydrate transport; plant carbon partitioning; manipulat carbohydrate distribution; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgcgtgctggccagctggctcaccgccttcgtcctcaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acctggctgctcatgtctgaggtcctgccctgcgtgcccgtggcgtggcctcagggctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccctggctcctcatgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcgcaggccgcaaggtgctgctcttcgtctcaggctacgtcgtggggctggggtcccatc 60
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                                                                                                                                                                                                                                                                                                                       Lightner JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; neuroprotective; antidepressant; nootropic; ian; and immunostimulant. The proteins and polynucleotides can be used in gene therapy, antisense therapy and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0081131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US07561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 A; 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA; 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.5%;
                                                                                                                                                                                                                                                                                                                          Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74.6; DB 2
Pred. No. 2.3e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbon partitioning; manipulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 T; 0 other;
                                                                                                                                                                                                                                                                                                                       Thorpe CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurodegenerative
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The present sequence encodes part invention, which describes hexose

of a hexose carrier protein from carrier proteins isolated from

from

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PARRAR PRARRAR PRARRAR
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Best Local Similarity
25 FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

21-APR-1999

23-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic pathway; promoter; termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC42332 standard; DNA; 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1559 catcatgaccgtctttatcgc 1579
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                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       2000EP-0301439
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99US-0126264.

99US-0127462.

99US-0128334.

99US-0128714.

99US-01289714.

99US-0130077.

99US-0130449.

99US-0130510.
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99US-0123180.
99US-0123548.
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52.9%;
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Pred. No. 4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence;
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Best Local
                                            07-APR-2000;
        (HESK-) HESKA CORP
                           09-APR-1999;
                                                                                                   Ctenocephalides felis
                                                                                                                          Cat flea; hindgut and Malpighian tubule nucleic acid; HMT; flea infestation; vaccine; antiparasitic; therapeutic target;
                                                                                                                                                    Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1543
                                                                19-OCT-2000
                                                                                   WO200061621-A2
                                                                                                                       diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.4; DB 21; Pred. No. 5.2e-08; D; Mismatches 116;
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function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and antiagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antiagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (BLISA)). The present sequence represents a cat flea HMT cDNA of the invention.
                                                                                                                                                                                                                                       used to produce an HMT or HNC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and function of the proteins and their role in metabolism. The HMT and HNC
                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HNC) tissue. The invention also relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; Page 753-754; 964pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids useful infestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins. The invention additionally encompasses expression
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Sequence 554 BP; 115 A; 120 C; 143 G; 176 T; 0 other;

Query Match
Best Local Similarity
Matches 115; Conserv

Conservative

0;

64; 21;

19.4%;

Score 54.6; DB 21 Pred. No. 1.6e-06;

Length

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;

Arabidopsis thaliana DNA fragment SEQ ID NO: 48015

18-OCT-2000

(first entry)

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Sequence 23, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 45, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 31, Appl	Sequence 31, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

## ALIGNMENTS

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APPLICANT: Bogan, Jonathan S.

APPLICANT: Lodish, Harvey F.

APPLICANT: Lodish, Harvey F.

TITLE OF INVENTION: Method of Measuring Plasma Membrane
TITLE OF INVENTION: Targeting of GLUT4

FILE REFERENCE: 0399.1210-004

CURRENT APPLICATION NUMBER: US/09/591.025

CURRENT FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/154,078

PRIOR APPLICATION NUMBER: 60/138,237

PRIOR FILING DATE: 1999-06-09

NUMBER OF SEO ID NOS: 8

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US-09-591-025-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FAS: SEQ ID NO 8
LENGTH: 2592
TYPE: DNA
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sim
Matches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09591025 Patent No. 6303373
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
  1656
                                                                                                                                                      1536
                                                                                                                                                                                                                            1476\ {\tt catctttggcttcgtggcattttttgagattggccctggccccattccttggttcatcgt}
                                                                            1596
                                      228
                                                                                                                                                                                          108
                                                                                                                                                                                                                                                 48 catgtgcctcttcatcgctggttttgcagtaggctggggacccatcccctggctcctcat 107
                      ctacggcgcctt
                                                                                                                                                                      gtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtgtcctcaccaa 167
ctacgtcttcct 1667
                                                                        ctggacgagcaacttcatcattggcatgggtttccagtatgttgcggaggctatggggcc 1655
                                                                                                ctggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctcagacc
                                                                                                                                                  ggccgagctcttcagccagggaccccgcccggcagccatggctgtggctggtttctccaa
                                                                                                                                                                                                                                                                                                                             Similarity
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51.0%;
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                                                                                                                                                                                                                                                                                                       Score 41.6; DB 4;
Pred. No. 0.011;
0; Mismatches 94
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RESULT 2 US-08-957-130-12

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US-08-677-734A-8
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                                                                                                                 RESULT
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                                              Sequence 8, Application Patent No. 5871919
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 12, Application US/08957130
Patent No. 6290959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 737-35
INFORMATION FOR SEQ ID NO:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                435 CTCG 438
                                                                                                                                                                                            240 ctgg 243
                                                                                                                                                                                                                            375 CTATATGGTGTCCAACCCGTCCCTGATCACCAAGCAGATGTTGACATTCTATAGTGCAGA 434
                                                                                                                                                                                                                                            180 ctttctggtgaccaaagagtttaacagcatcatggagatcctcaggaccctacggcgcctt 239
                                                                                                                                                                                                                                                                                         315 CATGCTCATCATCTACATCTTTGAGTGCGCCTCCTGCATCACGTCCTACACCCCACCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
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                                                                              Application US/08677734A
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               Brant, Steven R. Yun, Chris C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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(202) 737-3528
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Donowitz, Mark
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                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                         Sequence 1, Application US/08366276 Patent No. 5534409
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                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       APPLICANT:
                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       APPLICANT:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Cloning, Tissue Distribution,
TITLE OF INVENTION: Functional Analysis Of The Hur
TITLE OF INVENTION: NHE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 tettecetetgeacateaagggtgtggetaceggegtetgtgteeteaceaactggttea 175
                                                                                                                                                                                                                                                                                                                                470 CCACCGGGCTGTCCCTCTACGGCGTCTTCCTCAGTGGGCT 509
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                                                ADDRESSEE: Cibn __
CMDREST: 7 Skyline Drive
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CITY: Washington
                                CITY: Hawthorne STATE: New York
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nes 83; Conservat
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TOPOLOGY: lir
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REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/677,734A FILING DATE: 10-JUL-1996
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10532
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DEDNESS: single
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                                                                                                                                                     Groner, Bernd
Gouilleux, Fabrice
Wakao, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 I Street, N.W., Suite 700
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                                                                                CIBA-GEIGY Corporation
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51.9%;
                                                                                                                      Cytokine Regulated Transcription Factor 12
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CURRENT APPLICATION DATA:

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STALL.
COUNTRY: U.2313-0299
ZIP: 22313-0299
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5670367
GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGE
APPLICANT: FALKNER, F.
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 5
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TELECOMMUNICATION INFORMATION:
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NAME: Elmer, James Scoot
REGISTRATION NUMBER: 36,
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APPLICATION NUMBER:
FILING DATE: 11-MAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 tctgtgtcctcaccaactggttcatggcctttctggtgaccaaagagtttaacagcatca 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 tggagatcctcagaccctacggcgccttctggctcaccgctgccttctgtatcc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 244..2625
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 teceetggetecteatgteagagatettecetetgeacateaagggtgtggetaeeggeg 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2818 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCGGGGCCTGACCAAGGAGAACCTGTTGTTTCTGGCGCAGAAGCTGTTCAACAACAGCA 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGTGGCCGCAGCTGTGCGAGGCGCTCAACATGAAATTCAAGGCCGAGGTGCAGAGCA 1807
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                                                                                                                                                                                                                                                                                                                                                                          E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : (919) 541-8614
(919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHEIFLINGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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50.6%;
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                                                                     Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                        Sequence 1, Application US/08363255 Patent No. 5783386
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                          APPLICANT:
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CLONE: pTZgpt-
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LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                        CORRESPONDENCE ADDRESS:
                                                                                      TITLE OF INVENTION:
                                                                                                                APPLICANT: PASCOPELLA, LISA APPLICANT: KAWAKAMI, RIKU P.
                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                   1288 YYY 1290
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
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STATE:
               CITY:
                         ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
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              Palo Alto
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California
                                                                                                                                              COLLINS, DESMOND M. de LISLE, GEOFFREY W.
                                                                                                                                                                            JACOBS, Jr., WILLIAM BLOOM, BARRY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)683-4109
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                                                                                    MYCOBACTERIA VIRULENCE FACTORS AND NOVEL METHOD FOR THEIR IDENTIFICAT
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4.5%;
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US-08-363-255-13/c
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                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                             Sequence
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Best Local Similarity 45.0
114; Conservative
                                                                                                                                                                                                  GENERAL INFORMATION:
                                              APPLICANT: COLLINS, DESMOND M.
APPLICANT: de LISLE, GEOFFREY W.
APPLICANT: PASCOPELLA, LISA
APPLICANT: KAWAKAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                            APPLICANT: JACOBS, Jr., WILLIAM APPLICANT: BLOOM, BARRY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1167 TGCGGCTTC 1159
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           1287 CTCGAGGTCATCGAGGTTGAGGTCGGCGGCGTCAAGGTCGAGGTCCTCGCCGGGCTCGAC
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ADDRESSEE: MOKRIGO...
CTRRET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                     190 accaaagagtttaacagcatcatggagatcctcagaccctacggcgccttctggctcacc 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-100
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCTCCTCGTCGTCATCGGCGGTCTGGCCGGGCGGCGGCGGCCGCCTCAGCTTCGAGGTC 1348
                                                                                                                                                                                                               3, Application US/08363255
5783386
                           MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 494-0792
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835..2424
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45.8%;
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                                                                                                                                                                                                                                                                                                            Query Match 11.7%;
Best Local Similarity 45.8%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2745 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
     1167
                                                               1227
                                                                                                            1287 CTCGAGGTCATCGAGGTTGAGGTCGGCGGGGGTCAAGGTCGAGGTCCTCGCCGGGGCTCGAC 1228
                                                                                                                                                                         1347 TTCGTGGTCTTCGTCGTCGCCCGAGTCGAGGTCGTCGTCGGCGTCGGCGCGCCACGTCGTC 1288
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OTHER INFORMATION: /note= "
OTHER INFORMATION: If it :-
                                                                                                                                                                                                                                       1407 GATCTCCTCGTCGTCATCGGCGGTCTGGCCGGGCGGCGACGGCCGCCTCAGCTTCGAGGTC 1348
                            250 gctgccttc
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                                                                                                                                 130 atcaagggtgtgggtaccggcgtctgtgtcctcaccaactggttcatggcctttctggtg 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                     70 titigoagtaggotggggacocatococtggotoctcatgtcagagatottccototgcac 129
                                                                                                                                                                                                                                                        10 gatgttcacctggggctggcctggctggctgtaggcagcatgtgcctcttcatcgctggt 69
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_difference
LOCATION: replace(2591, "")
OTHER INFORMATION: /note= "This position is C
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_difference
LOCATION: replace(2384, "")
OTHER INFORMATION: /note= "This position is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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SOFTWARE: Patenti
                                                                    accaaagagtttaacagcatcatggagatcctcagaccctacggcgccttctggctcacc 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
TGCGGCTTC 1159
                                                GTCGAGGTCTGGTTCAGCGTCGAGCTCCTCGACGGAGTCCAGGGCGTCCTCGGGGATCCGT 1168
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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If it is G the amino acid translation
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                          Mismatches 135;
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US-09-178-973B-7

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; LOCATION: (268)..(1446)
US-08-956-998-1
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                                                                                                                                               Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 1
LENGTH: 1635
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/956,998
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 2
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APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (TIFS)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pachuk, Catherine APPLICANT: Herold, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Vaccines FILE REFERENCE: AHP27USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                           ORGANISM: Herpes simplex virus type FEATURE:
689 ccgagtgcccctacaacaagtcgttgggggtct 721
                     149 gcgtctgtgtcctcaccaactggttcatggcct 181
                                                                       629 ccatcgcctggtatcgcatgggagacaattgcgctatccccatcacggttatggaataca 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 tgtcaga 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 actcagcaatcagctcagctcctgtcacatcagcggtgacgaccagaacatccagaagaa 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 cctcaccaactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagat 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 gctccccagtcagacaggttccagccctacatgcaggaggtggtacctttcctgaccaa 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 68; Conserv
                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 gctcctcatgtcagagatcttccctctgcacatcaagggtgtgggctaccggcgtctgtgt 158
                                                                                           ccatcccctggctcctcatgtcagagatcttccctctgcacatcaagggtgtggctaccg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                       Conservative
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53.5%;
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                                                                                                                                                   Score 32.2; DB Pred. No. 3.5; 0; Mismatches
                                                                                                                                                     0;
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Pred. No. 2.5;
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US-09-087-465-9
Sequence 9, Application US/09087465A
Patent No. 6160092
GENERAL INFORMATION:
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US-08-393-333-1
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Best Local Similarity 50.7%;
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMBON, RICHBIE A 6, REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      1565
                                                                                                                                                                                                                                                                               1505
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LENGTH: 2385 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1999 TELEFAx: (415) 398-3249 TELEX: 910 277299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                               1625 GCAGCCACCTGGAGGACTACAGTGGCCTGT 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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                                                                                                                                                          212 tggagatcctcagaccctacggcgccttct 241
                                                                                                                                                                                                                                       152 tetytyteeteaceaactgytteatgycetttetyytyaecaaagagtttaacagcatea 211
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                             TGCTGTGGCCGCAGCTGTGTGAGGCGCTCAACATGAAATTCAAGGCCGAAGTGCAGAGCA 1564
                                                                                                                                                                                                      ACCGGGGCCTGACCAAGGAGAACCTCGTGTTCCTGGCGCAGAAACTGTTCAACAACAGCA 1624
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Hou, Jinzhao
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Pred. No. 5.6;
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APPLICANT: Vinkemeier, Uwe APPLICANT: Chen, Xiaomin APPLICANT: Darnell Jr., James

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US-08-466-603-4/c
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TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS:
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-229
CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 3714
TYPE: DNA
ORGANISM: Homo sapiens
US-09-087-465-9
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Patent No. 572601
                                                               INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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                                               SEQUENCE CHARACTERISTICS:
                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               FILING DATE: 06-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pasternack, Gary R. APPLICANT: Kuhajda, Francis P. TITLE OF INVENTION: NO. 572601 TITLE OF INVENTION: Uncontroll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1682 gcagccacctggaggactacagtggcctgt 1711
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                                                                                                                            NAME: POSOTSKE ESQ., Laurence H
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.4:
                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1001 G Street, N.W. CITY: Washington, D.C. STATE: District of Columbia
                               LENGTH:
                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                 : 759 base pairs
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                                                                                 202 508-9299
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                                                                                                                                                                                                                                                                   06-JUN-1995
double
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Francis P.

No. 5726018el Mammalian Protein Associated With Uncontrolled Cell Division
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                                                                                                                              1107.47218
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Pred. No. 6.2;
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                                                                                                                                                               TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08314503A Patent No. 5734022
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Best Local S
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                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
                                               FEATURE:
                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: POSOTSKE ESG., Laurence H.
REGISTRATION NUMBER: 34,698
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
                             NAME/KEY:
                LOCATION:
                                                             ORGANISM:
                                                                                                           TOPOLOGY:
                                                                                                                      STRANDEDNESS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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1 Similarity 52.3%;
69; Conservation
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T: 1001 G Street, N.W.
Washington, D.C.
                                                                                                                                     nucleic acid
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                                                                                                                                                    759 base pairs
                                                           Mus sp
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Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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 Query Match 11.3
Best Local Similarity 52.3
Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: 202 508-9153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                    FEATURE:
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ZIP: 200
                                                                                                 NAME/KEY:
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                  NAME: Posorske Esq., Laurence H. REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/314,503 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/468,066 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                   STRANDEDNESS:
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52.38;
                  11.1%;
52.3%;
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Score 31.2; DB: Pred. No. 5.6; 0; Mismatches
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                                DB 1;
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US-08-466-717-4
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; Patent No. 5874234
                                                  Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pasternack, Gary R.

APPLICANT: Kuhajda, Francis P.

TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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150 cgtctgtgtcctcaccaactggttcatggcctttctggtgaccaaagagtttaacagcat 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Posorske Esq., REGISTRATION NUMBER:
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STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                              ORGANISM:
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BG3225106 602422555
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BG700749 602681616
AL534131 AL534131
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C88387 C88387 Carp
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BE598634 P11.84_B0
AV524951 AV524951
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Contact: Lee, NH
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability please contact
(tdbinfo@tdb.tigr.org)
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Comparative expressed-sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
                                                                                                                                                                                                                                                                                                                                                                                     H34451 319 bp mRNA EST EST111406 Rat PC-12 cells, NGF-treated (9 days) Ra end similar to Glucose transporter, mRNA sequence.
                                                                                                                                                                                Proc. Natl. Acad.
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Mammalia; Eutheria;
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/organism="Rattus sp."
/db_xref="ATCC (inhost):2005510"
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Rodentia;
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Sciurognathi; Muridae; Murinae;
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FEATURES
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High quality sequence stop: 644.
Location/Qualifiers
                                                                                                                                                                   Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9192 row: d column: 12
                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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601757442F1 NCI_CGAP_Mam5
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/organism="Mus musculus"
/strain="C57/B6"
/db.xref="taxon:10090"
/clone="IMAGE:3986651"
/clone_lib="NGI_CGAP_Mam5"
/tissue_type="tumor.gross t
/dev_stage="7 months"
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/clone_lib="Rat pC-12 cells, NGF-treated (9 days)"
/note="Wector: pBBuescript SK-; Site_1: EcoR; Site_2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. CDNA was constructed using an oligo-dT primer
and directionally cloned using the Lambda ZAP II Vector
Kit by Stratagene"
80 g 88 t 1 others
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99.3%;
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Pred. No. 5.2e-61;
0; Mismatches 2
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Sciurognathi; Muridae; Murinae; Mus
             tissue"
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Best Local (
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                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 70 row: A column: 21
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136437 MARC 1PIG :
BE231636
BE231636.1 GI:90:
                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                            USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                     Contact: Smith TPL
                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                EST discovery in swine
                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA
                                                                                                                                                                                                                                                                                                              and Keele, J.W.
                                                                                                                                                                                                                                                                                                                            Fahrenkrug, S.C. Stone, R.T., Hea
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 546)
                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                         /organism="Sus scrofa"
                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Heaton, M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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on,M.P., Grosse,W.M., Benne
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Pred. No. 2.8e-47;
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BG749509
BG749509.1 GI:14060162
EST.
                                                                                                                                                                                                                             High
                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryola: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG749509 949 bp mRNA EST 602707648F1 NIH_MGC_43 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 949)
                                                                                                                                                                                                                            quality sequence stop:
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                                                                                                                                                                                                                                            LLCM1681 row: p column:
/tissue_type="normal pigmented retinal epithelium" /lab_host="pH10B (phage-resistant)" /note="Df10B (phage-resistant)" /note="Organ: eye; Vector: pOTB7; Site_1: xhoI: Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(3). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Library made from pooled tissue from day 11, 13, 1 and 30 embryos."

a 182 c 162 g 124 t 2 others
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                        /clone_lib="NIH_MGC_43"
                                                                                                                                         /clone="IMAGE:4844411"
                                                                                                                                                                                                             Locati
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86.8%;
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I. NO. 2.3e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 934)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
Unpublished (1999)
                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: J.LAM9706 row: i column: 01
                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BE910478
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601501005F1 NIH_MGC_70
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Eukaryota; M
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                 143
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                                  Average insert size 1.1 kb. Technologies."
                                                            /tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage resistant)"
/note="Organ: pancreas; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHH_MGC Library. | "
302 c 264 g 223 t
                              Technologies
                                                                                                                           /clone="IMAGE:3903048"
/clone_lib="NIH_MGC_70"
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1.2e-45;
Pred. No. 1.3e-45;
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               9
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BG290178
BG290178.1 GI:
                                                                                                                                                                                                                                        High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60290178 712 bp mrNA EST 21-FEB-2001 602385265F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4514200
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                  117
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                                                                                                                                                                                                                                                                          LLAM10402 row: a column:
/clone="mange::514200"
/clone=lib="NHH_MGC_93"
/clone=Lib="NHH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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84.8%;
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Pred. No. 1.3e-40;
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Query Match Best Local Similarity

66.7%;

Score 188.2; DB 11; Pred. No. 8.1e-38;

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC colone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Washingtion Genome Center
DRAAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.renome.washingtion.de.do.
                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 415.
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presence of a XhoI site followed
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Other_ESTs: 2820759.5prime
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DHIOB (phage-resistant)"
//lab_host="DHIOB (phage-resistant)"
//note="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                                                                               /organism="Homo sapiens
/db_xref="taxon:9606"
/clone="IMAGE:2820759"
                                                                                                                                                                   /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                        /clone_lib="NIH_MGC_7"
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                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and
v0.980904.e. Vector identified by cross_m
                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
Tel: 402 762 4366
Fax: 402 762 4390
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/note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fet
                                               /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                               Location/Qualifiers
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AL565390
                                                                                                                                                                                                                                                                                                                                                                                                                             BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, \u00e4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 752)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                       PUMVSFORT 6 Vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@litetech.com URL: fliang@litetech.com URL: http://fulllength.invitrogen.com" 9 others
                                                                                                                                                                                  /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                             week, 24 week and 26 week)"

/lab_host="DH10B"

/note=""Orange"
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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141 c
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80.1%;
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87.3%;
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Pred. No. 1.7e-32;
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                DB 10;
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Conservative

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                                                                                                                                                                                                                          Seq primer: T3 POLYA=No.
                                                                                                                                                                                                                                                    FORWARD: T3
BACKWARD: T7
                                                                                                                                                                                                                                                                              This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                             Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG672321
DRNCFD10
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     induced by peripheral nerve axotomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Distinct gene expression profiles of rat dorsal root ganglion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiao,H.S.,
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EST.
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Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G., Chen,Z.
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                                                                                                                                                                                                                                                                                                                                             xu.zhang@ion.ac.cn
                                                           /tissue_type="dorsal root ganglion"
/dev_stage="adult"
146 c 138 g 136 t
                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                      /clone="DRNCFD10"
/clone_lib="Rat DRG Library"
                                                                                                              /sex="male"
                                                                                                                                                                                                          Location/Qualifiers
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                    CCTCCGGCCCTACGGCGTTCTGGCTCGGCCTCTGCCTTCTGCATCTTCGGCGTCCTTTT
                                      cotcagaccotacggcgccttctggctcaccgctgccttctgtatcctcagcgtcctttt 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin Luther University Halle-Wittenberg, Med Grosse Steinstrasse 52, D-06097 Halle, GERWANY Email: sike.kietz@gmx.de
                                                                                                                                                                                                                                           Similarity
281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kietz S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
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Expression of glucose transporters i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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(bases 1 to 235)
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                                                                                                                                                                                                                                                                                                                             39
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                                                                                                                                                                                                                                                                                                                                                                        /Organism="Oryctolagus
/strain="hybrid strain
/db_xref="taxon:9986"
/clone="G81"
                                                                                                                                                                                                                                                                                                                      /dev_stage="six days old preimplantation 78 \text{ c} 61 \text{ g} 57 \text{ t}
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="rabbit blastocyst mRNA to cDNA"
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88.5%;
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Matches 185
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tgtcctcaccaactggttcatggcctttctggtgac-caaagagtttaacagcatcatgg
                                                         CTGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGGCTGGCGACAGGCATCTG
                                                                                                                                                             99ctgtaggcagcatgtgcctcttcatcgctggttttgcagtaggctggggacccatccc 95
                                                                                ctggctcctcatgtcagagatcttccctctgcacatcaagggtgtgqctaccggcgtctg 155
                                                                                                                                          GCCAGTGGGCAGCATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGGGGGCCCCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rua Prof. Antonio Pru
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                         al Similarity
185; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BF742266
BF742266.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                      /note-*Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone_lib="BTN0409"
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http://image.llnl.gov
Plate: LLAM9259 row: a column: 06
High quality sequence stop: 605.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
Clone distribution: NCI-CGAP clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF140667 917 bp mRNA
601786917F1 NCI_CGAP_Lu30 Mu:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oli dT. Library constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                            Investigator providing samples: Gilbert Smith, 263 c 277 g 214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4014605"
/clone_lib="NCI_CGAP_Lu30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Rodentia;
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Pred. No. 6.6e-28;
Pred. No. 6.8e-28;
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Best Local Similarity 91.8
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                                                                     source
                                       61
                                                                                              atcgctggttttgcagtaggctggggacccatcccctggctcctcatgtcagagatcttc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3037 row: C column: 03
Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verification and initial annotation of NIA mouse 15K cDNA clone set Unpublished (2001) Other_ESTs: H3037C03-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 595)
Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K.,
,T.S., Carter,M.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG079217 595 bp mRNA EST 26-JAN-2001
H3037C03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3037C03 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                         clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastcocyst, embryosic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos or and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dr)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 127: 1737-1749; (3) Genome-wide mapping of 7.5-day mouse embryos reveals entrembryonic tissue of and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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/clone="H3037C03"
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/strain="C57BL/6J"
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Pred. No. 6.6e-25;
0; Mismatches 13
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                                                                                                                                                                                                                    Length 595;
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                                                                                                                                                                       0;
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Qy

Дb

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204 cagcatcatggagatcctcagaccctacgg

CAGCCTCATGCTCCTGCTGCTGCTCTGAGG

QУ

144 taccggcgtctgtgtcctcaccaactggttcatggcctttctggtgaccaaagagtttaa 203

GACAGGCATCTGCGTCCTCACCAACTGGCCTCATGGCCTTTCTCGTGACCAAGGAGTTCAG

236

233 206

В QУ

Matches 124;

Local

Similarity

38.4%;

Score 108.4; DB 1 Pred. No. 1.2e-17; Mismatches

DB 10;

Length

358;

0; Gaps

0;

Conservative

0;

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BASE COUNT
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nq49d04.sl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 507 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 507 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 350)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.'
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution
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AA627408.1
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                    87
                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 349
                                /note="organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4). "
     vector. Library is normalized. Library was con:
Bento Soares and M. Fatima Bonaldo (N-Soares4).
a 104 c 101 g 66 t
                                                                                                                                                                                                                            /tissue_type="colon tumor RER+"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                          /clone="IMAGE:1147207"
/clone_lib="NCI_CGAP_Co10"
                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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Search completed: February 13, 2002, 13:37:42 Job time: 2989 sec

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Compugen Ltd

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Copyright (c) 1993 - 2000 Comp
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321.379 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB		1D	Description
1	2310.5	99.4	477	22	AAE04888	Human transporter
2	2301.5	99.0	477	22	AAB66932	Human GLUTXI. HOM
اند	2104	90.5	478	22	AAB66939	GLUTXI COnsensus s
4	2057	88.5	478	22	AAB66933	RAT GLUTAI. Karru
رت ر	2041.5	87.8	477	22	AAB66934	Murine Groiar, Mu
6	1007.5	43.4	262	22	AAE06579	Human procern nave
7	953	41.0	503	22	AAB66938	Kar Ghoisa. Nacca
8	930	40.0	507	22	AAB66941	GLOTAS CONSCISUS S
9	927	39.9	507	22	AAB66937	Hullian ordivation
10	657	28.3	437	21	AAG13750	Aldolucia chalia
11	657	28.3	447	21	AAG13749	Arabidopais charia

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AA149025	1000	3 D11360	2020	א ני ני	771	AAG48644	AAG48645	AAG48646	AAY27290	AAB13225	AAG50066	AAG16798	AAG52315	AAB66936	AAY49633	AAWI/836	AAY50/99	AAB6694U	AAB66935	AAG39281	AAG39282	AAG15414	AAG15415	AAG15416	AAB30522	AAY27292	AAY27289	AAG38869	AAG388/U	AAG38871	AAG20976	AAG20977	AAG20978	AAG13/48	1
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## ALIGNMENTS

AAE04888 RESULT ۲

AAE04888 standard; Protein; 477 AA

AAE04888;

10-SEP-2001 (first entry)

Human transporter and ion channel-1 (TRICH-1) protein.

Human; transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; plck's disease; bachaemic cerebrovascular disease; ADDS; anxiety; stroke; Huntington's disease; parkinson's disease; cerebral neoplasm; allergy; Huntington's disease; mental disorder; Schizophrenia; polymyositis; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract, myocarditis; Grave's disease; cerematomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; mallabsoration sundromae, buccarrichaemae; and disorder; disease; mallabsoration sundromae, buccarrichaemae; and disorder; disease; mallabsoration sundromae. malabsorption syndrome; hypercholesterolaemia;

## Homo sapiens

Domain	Domain	Domain	Key Domain
320339	293313 /label= Transmembrane_domain	259279 /label= Transmembrane_domain	Location/Qualifiers 29474 /note= "Sugar transporter domain"

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                                                                                                                                                                                                                                                       C disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar c disease, dementia, depression, epilepsy, ischaemic cerebrovascular c disease, stroke, cerebral neoplasms, Pick's disease, Huntington's c including mood, anxiety, Schizophrenia and seasonal affective disorders c muscle disorder including cardiomyophrenia and seasonal affective disorders c including sarrhythmias and asthma and immunological disorders. C dermatomyositis, arrhythmias and asthma and immunological disorders c including AIDS, adult respiratory distress syndrome (ARDS), allergies, c syndrome, systemic lupus erythematosus and other diseases including c sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary c sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary c glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                    Matches
144 \cdot y isei ay pavr gll gscvqlmvvvgill ay lagwvlewrwlavlgcvppslmlllmcfmp
                                                                                                                                                                                                                                                    Sequence
             121 YISEIAYPAVRGLIGSCVQLMVVVGTLLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is transporter and ion channel-1 (TRICH-1) protein TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 112-113; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human transporter and ion channel
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Tang YT, K
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10-FEB-2000;
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28-JAN-2000;
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14-JAN-2000;
                                                                                                                                                                                             Local Similarity
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                                                                     GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120
                                                        gvlggwlvdragrklslllcsvpfvagfavitaaqdvwmllggrlltglacgvaslvapv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing transport, neurological,
prders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as transport disorder including amyotrophic lateral sclerosis, ic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
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, Azimzai Y,
                                                                                                                                                                               Conservative
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2000US-0177332.
2000US-0178572.
2000US-0179758.
2000US-0181625.
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Yue H, Nguyen
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Pred. No. 4.3e-224;
1; Mismatches 0; I
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DB,
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Gandhi
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               The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is human GLUTX1.
                                                                                                                                                                                                                                                                14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
                                                                                                            Claim 11;
                                                                                                                                           the
                                                                                                                                                                                     WPI;
                                                                                                                                                    Nucleic
                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                (UYLA-)
                                                                                                                                                                                                                                                    13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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                                                                                                                           leic acids encoding GLUTX glucose transporter proteins, useful in prevention, diagnosis and treatment of hexose transport disorders, ischemia and diabetes -
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                                                                                                                                                                                    2001-112615/12
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99US-0151140.
2000US-0184285.
2000US-0616132.
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The present sequence is human GLUTX1

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RESULT
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Best Local Similarity
                                                                                    14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
  Nucleic acids
                                                                                                                                                                                 W0200104145-A2
                                                                                                                                                                                                                                                                                        GLUTX1 consensus
                                                                                                                                                                                                                                                                                                                                                       AAB66939 standard;
                                                                (UYLA-)
                                                                                                                                        14-JUL-2000;
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                                                                                                                                                                                                                                               hypoglycaemia;
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transport disorder; ischaemia; diabetes; hyperglycaemia;
ycaemia; glucose metabolism disorder; neurodegenerative d
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e.g. ischemia and diabetes
                                                        Claim
                                                       Page 74-75; 124pp; English.
                                                                      diagnosis and treatment
                                                                       of
                                                                       hexose transport disorders,
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The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence hyperglycaemia, hy neurodegenerative for GLUTX1. Sequence AA: Length 478; sequence and

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          LASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR
                                                                               alsgvimvfsmsafgtyfkltqsgpsnsshvgilvpisaepvdvsvglawlavgsmclfi
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                                                  AGFAVGWGPIPWLLMSEIFPLHVKGVATGTCVLTNWLMAFLVTKEFSSLMEVLRPYGAFW 418
                                                                                                                                          LMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLL
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                                                                                                                      lmvfqqlsgvnaimfyantifeeakfkdsslasvtvgiiqvlftavaalimdragrrlll
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pred. No. 2.7e-203;
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17-APR-2001

entry)

Rat GLUTX1

AAB66933

standard;

Protein;

478

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18-JAN-2001 WO200104145-A2

qs

Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative d

disease

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27-AUG-1999;
23-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g.
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                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          leic acids encoding GLUTX glucose transporter proteins, useful in prevention, diagnosis and treatment of hexose transport disorders, ischemia and diabetes -
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                                                                                                                                                                                                                                                  AGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFW 418-
                                                                                                                  alsgvimvfsmsafgtyfkltqsgpsnsshvgllvpisaepadvhlglawlavgsmclfi
                                                                                                                            VLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFI
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                                                                                 agfavgwgpipwllmseifplhikgvatgvcvltnwfmaflvtkefnsimeilrpygafw
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                                                                                                                                                                                           ETPRFLLTQHRRQEAI-ALRFLWGSEQGWEDPPIGAE-QSFHLALLRQPGIYKPFIIGVS
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)B; AAF55866.
                                                ltaafcilsvlftltfvpetkgrtleqitahfegr
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99US-0151140.
2000US-0184285.
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85.7%;
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Pred. No. 1.4e-198;
2; Mismatches 31;
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AAB66934

standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes \dot{}
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                      299
                                                                                                                                                                                                                                                                                                                   VLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFI
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391; Conserv
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Pred. No. 5.3e
32; Mismatches
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06-JAN-2000;
11-JAN-2000;
                                                                                                                                               HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA
                                                                                                                                                                                                                                                                                                                      Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, {\bf Alz}{\bf heimer's} and inflammation -
               supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate
                                                                                  probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodic and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional
                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                       present sequence is human
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                                                                                                                                                                                                                                                                                      1; Page 75;
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e; antiinfertility; antiinflammatory.
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growth activity (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disorder; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemotactic; chemokinetic;
                                                                                                                  antibodies
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RESULT
AAB66938
QΥ
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Best Local
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                                                                                                Claim 11; Page 82-83; 124pp; English.
                                                                                                                                                    the prevention, diagnosis and treatment e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-IB01042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia hypoglycaemia; glucose metabolism disorder; neurodegenerative of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2001
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                                                                                                                                                                                                       Nucleic acids encoding GLUTX glucose transporter proteins,
                                                                                                                                                                                                                                                                                                                                                                                   (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200104145-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-2000;
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DB; AAF55871.
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2000US-0184285.
2000US-0616132.
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                                                                                                                                                                                                                                                                                                                                   3
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                                                                                                                                                                            of hexose transport disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to inhibit tumour growth
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glucose carriers

GLUT1-GLUT5

and have hexose binding and/or

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative

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RESULT
AAB66941
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XX AAB6
XX AAB6
AC AAB6
XX AAB6
XX AAB6
XX AAB6
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             14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                                                                                           GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypeglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX3.
                                                                                 14-JUL-2000;
                                                                                                             18-JAN-2001
                                                                                                                                         WO200104145-A2
                                                                                                                                                                      Rattus
                                                                                                                                                                                                                                                                     GLUTX3
                                                                                                                                                                                                                                                                                               17-APR-2001
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99US-0151140.
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Pred. No. 2.4e-87;
'9; Mismatches 168
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Human GLUTX3

entry!

Human; GLUTX; gene therapy; vaccine; hexose transport disorder; ischaemia;

; vaccine; hexose transport modulator; ischaemia; diabetes; hyperglycaemia; RESULT AAB66937

standard;

Protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETPRELLTQHRRQEAI-ALRELMGSEQG--WEDPPIG---AEQSEHL--ALLRQPGIYKP :|||||: | | | : | | | : :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFE-GR
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                                                                                                                         pagyltlvpllatmlfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvlt
                                                                                                                                                                                    SVG-LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVT
                                                                                                                                                                                                                                            mdlagrkvllfvsaaimfaanltlglyihf---gprrlspnstagleseswgdlaqplaa
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ksflpvvstfglqvpflffaaiclvslvftgccvpetkgrsleqiesffrtgr
                                                                                                                                                                                                                                                                                                       MDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS-----AQPVDA
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Pred. No. 5e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 81-82; 124pp; English.
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13-JUL-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
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             402 KEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFE-GR
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                                                                                                                                                                                                                                                                                                                         ne prevention, diagnosis and treatment of hexose.g. ischemia and diabetes -
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                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                               nsprfllsrgrdeealralawlrgtdvdvhwefgqiqdnvrrqssrvswaearaphvcrp
                                                                                                                                                                                                                                             YISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMP 180
                                                SVG-LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNNLMAFLVT 401
                                                                                                                                                          FIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF----KDSSLASVVVGVIQVLFTAVAALI
                                                                                                                                                                                              ETPRFLLTQHRRQEAI-ALRFLWGSEQG--WEDPPIG---AEQSFHL--ALLRQPGIYKP 232 :|||||: | || : | || : |
                                                                                                                                                                                                                               yvseiappgvrgalgatpqimavfgslslyalglllpwrwlavagxapvlimilllsfmp 215
                                                                                                                                                                                                                                                                                                       GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120
                                   pagyitlvpllatmlfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvlt 449
                                                                                    mdlagrkvllfvsaaimfaanltlglyihf---gprplspnstagleseswqdlaqplaa
                                                                                                          MDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS-----AQPVDA 342
                                                                                                                                  itvallmrllqqltgitpilvylqsifdstavllppkdd---aaivgxvrllsvliaalt 332
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99US-0151140.
2000US-0184285.
2000US-0616132.
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44.2%; Pred. No. 1e-84;
vative 78; Mismatches 1
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04-JUN-1999;
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10-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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27 - MAY - 1
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24-MAY-1
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18-MAY-1
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05-MAY-1999
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01-APR-1999;
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25-MAR-1999;
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19-APR-1999
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            990S-0134941
990S-0135124
990S-0135629
990S-0136021
990S-0136782
990S-0136782
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36.1%;
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  25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification; signal transduction pathway; metabolic
sation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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Pred. No. 1.3e-57;
2; Mismatches 170;
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                                                                        LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 122
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                                                                                                             ragrkplllvsatglvigcliaavsfylkv-----hdmaheav-----
                                                                                                                      RAGRRLLLVLS--GVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAW
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99US-0161406

99US-0161350

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99US-0161920

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99US-0161932

99US-0161932
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Pred. No. 8.8e-57;
2; Mismatches 171;
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Perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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US-09-299-549-10
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US-08-928-692-12
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US-09-031-392-3
US-09-031-392-7
US-09-040-444-1
US-09-040-444-1
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Best Local Similarity
Matches 149; Conserv
                   10 LIFAISIATIGSFOFGYNTGVINAPEAIIKDFLNYTLEERSETPPSSVLLTSLWSLSVAI
                                           3 VFLAAFAAALGPLSFGFALGYSSPAIPSL------QRAAPPAPRLDDAAASWFGAV 52
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ALIGNMENTS	US-08-471-496-9	US-08-6//-049-6	US-08-5//-049-/	PCT-US96-10986-14	US-08-494-907-14	US-09-231-818-21	US-08-510-6468-22	US-08-403-852D-21	PCT-0593-05704-0	US-U8-U63-JJZ 0	05-06-64/-39/-z	05-06-033 307-3	PCI = 0393 03704 7	DS-08 000 002 7	115-08-063-552-7	115-08-964-127-2	US-08-814-8//-4	US-08-944-910-4	US-08-850-880-4
	Seducince //		20 .	7 .		sequence 14. Appl	) t	22											

## US-09-031-392-5 Sequence 5, Application US/09031392 Patent No. 5942398 GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 35,283 REFERENCE/DOCKET NUMBER: 07334 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-8906 TELEFAX: 617/542-8906 TELEEX: 200154 TELEFAX: 617/542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: TITLE OF INVENTION: NUCLEIC ACID MOLECULES THEREOF APPLICANT: Tartaglia, APPLICANT: Weng, Xun SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett CORRESPONDENCE ADDRESS FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION: Anita L. NAME: Meiklejohn, Ph.D., Anita L. NUMBER OF SEQUENCES: TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE CHARACTERISTICS: OPERATING SYSTEM: SOFTWARE: FastSE( COUNTRY: USA ZIP: 02110-2804 STATE: STREET: 225 CITY: Boston APPLICATION NUMBER: US/09/031,392 COMPUTER: ADDRESSEE: LENGTH: : 494 amino acids amino acid MA E: Fish & Richardson P.C. 225 Franklin Street IBM Compatible Diskette Windows95 10 Louis A. 07334/072001

Conservative

24.6%; Score 571; DB 2; Length 494; 30.5%; Pred. No. 2.9e-47; tive 94; Mismatches 179; Indels

179; Indels 66;

Gaps

10;

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                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                 APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                              TELEX:
                 LENGTH:
                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                        NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110-2804
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            494 amino acids
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MOLECULE TYPE:
US-09-299-549-5
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
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                                                                 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
                  FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                               COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                             STATE: M
                                                APPLICATION NUMBER: US/09/031,392
                                                                                                                                                                                                                              STREET: 225 |
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 NWLMAFLVTKEFSSLMEVLRPYGAFWL-ASAFCIFSV-----LFTLFCVPETKGKTLEQ 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 MTISLLLKDNYSWMSFICIGAILVFVAFFEIGPGPIPWFIVAELFGQGPRPAAMAVAGCS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 APVSAQPVDASVGLAWLAVGSMCLFTAGFAVGWGPTPWLLMSEIFPLHVKGVATGICVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GAGVVNTIFTVVSVFLVERAGRRTLHLI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 FCGLCTGFVPMYIGEISPTALRGAFGTLNQLGIVIGILVAQIFGLKVILGTEDLWPLLLG 189
                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 ACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVL----EWRWLAVLG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 FSVGGMIGSFSVGLFVNRFGRRNSMLIVNLLAIAGGCLMGFCKIAESVEMLILGRLIIGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 VTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVI---TAAQDVWMLLGGRLLTGL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LIFAISIATIGSFQFGYNTGVINAPEAIIKDFLNYTLEERSETPPSSVLLTSLWSLSVAI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITRAFEGQ 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTILPAIIQCAALPFCPESPRFLLINRKEEEKAKEILQRLWGTEDVAQDIQEMKDESMRM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CVPPSLMLLLMCFMPETPRFLLTQHRRQEAI--ALRFLWGSEQGWEDPPIGAEQSFH- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LALLROPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASV 272
                                                                                                                                                                                                                                                                                                                                                                                                        0, Application US/09031392
5942398
Meiklejohn, Ph.D., Anita L.
                                                                                                                                                                                                               ΜA
                                                                                                                                                                                             USA
                                                                                                                                                                                                                                            225 Franklin Street
                                                                                   SYSTEM: Windows95
FastSEQ for Windows Version
                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                            Fish & Richardson P.C
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                                                                                                                                       Diskette
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Pred. No. 2.9e-47;
                                                                                   2.0
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US-09-299-549-10

: Sequence 10, Application US/09299549

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Best Local Similarity
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                                                                                                                                                                                                                 GENERAL INFORMATION:
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TOPOLOGY: line
NOLECHIE
                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: GLUTEX AND USES THEREOF NUMBER OF SEQUENCES: 10
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                          APPLICANT: Tarta
                                                                                                      CORRESPONDENCE ADDRESS:
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TELEFAX: U.L.,
TELEFAX: 200154
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               COUNTRY:
                                   STATE: MA
                                                      CITY:
                                                                    ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFG-----AVVTLGA- 57
                                                                                                                                                                                                                                                                                                                                            ETKGRTFDEIAAAF 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGGMAGCAVLMTIALALLDQVPWMSYVSIVAIFGFVAFFEVGPGPIPWFIVAELFSQGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQGWEDPPIGAEQSFH-LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETTFEEA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE----- 157
                                                                                                                                                                                                                                                                                                                                                                                                                  PAAIAVAGESNWTSNFIVGLLFQYIAELLGPY-----VFIVEAVLLLLFFIETFLKVP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFTAGFAVGWGPIPWLLMSEIFPLHVK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEMKDESRXMXSEKXVSVLELFRSRXYRQPVIIAIVLQLSQQLSGINAVFYYSTSIFEKA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESLWPLLLGLTGVPALLQLLLLPFCPESPRYLLI-NKNEEARAKKALQRLRGTADVSQEV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA---IALRFLWG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAVLIAALGSFQYGYNLGVIN-----APQKVIEAFYETWLGRXGEXPSVPTLTLL 65
02110-2804
                                                 Boston
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                  USA
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Weng, Xun
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ER: 07334/072001
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
455 ETKGRTFDETAAAF 468
                                                                       402 PAAIAVAGESNWTSNEIVGLLEQYIAELLGPY-----VEIVFAVLLLLEEIFTELKVP
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                                                                                                             383 GVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVL-----FTLFCVP 436
                                                                                                                                                                                                                             303 GVGQPVYATIGAGVVNTVFTVVSVFVVERAGRRTLHLL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meiklejohn, Ph.D. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07334/072002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFG-----AVVTLGA- 57
                                 ETKGKTLEQITAHF 450
                                                                                                                                                                                                                                                                 KFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLSVSIFAVGGMIGSFLVGXIGNRLGRKXAMLVNNVLAIAGGLLMGLAKXAXSFEMLIL 125
                                                                                                                                                                                     PGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRFIIGLYCGLSSGVVPMYVGEISPTALRGALGTLNQLGIVIGILIAQVLG--LDSLLGN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVLIAALGSFQYGYNLGVIN------APQKVIEAFYETWLGRXGEXPSVPTLTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AAGGVLGGWLV----DRAGRKLSLLLCSVPFVAG---FAVITAAQDVWMLLG 102
                                                                                                                                                 \tt LGGMAGCAVLMTIALALLDQVPWMSYVSIVAIFGFVAFFEVGPGPIPWFIVAELFSQGPR
                                                                                                                                                                                                                                                                                                     AEMKDESRXMXSEKXVSVLELFRSRXYRQPVIIAIVLQLSQQLSGINAVFYYSTSIFEKA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                   401
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RESULT 5 US-08-928-692-13

Sequence 13, Application US/08928692 Patent No. 5958727

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Best Local Similarity 28.6
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
           424
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                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                       374
                                                                                                      269
                                                                                                                       314 GKNVPEKVWNTIKELHTVPSNLRALIIGCGLQAIQQFTGWNSLMYFSGTIFETVGFKNSS
                                                                                                                                                                                    260 FTCLCFLPDTPRYYVMKGDLARATEVLKRSYTDTSEE-----IIERKVEELVTLNQSIP
                                                                                                                                                                                                           173 LLLMCFMPETPRFLLTQ----HRRQEAIALRELWGSEQGWEDPPIGAEQSFHLALLRQ--- 226
                                                                                                                                                                                                                                                                                            118
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                                                                                                                                                                                                                                                                                                             140 LITSIFAGTAADIFGRKRCLMGSNLMFVIGAILQVSAHTFWQMAVGRLIMGFGVGIGSLI 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICALION.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods for modifying the Production NUMBER OF INVENTION: a Polypeptide NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           58 AAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLV 117
                                                                                                                                                                                                                                                                                                                                                                          86 IITLTFVASISGFMFGYDTGYISSALISI-----GTDLDHKVLTYGEKEIVTAATSLGA
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TOPOLOGY: lin
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TELEPHONE: 212-878-9655
TO TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                        3 VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASW-----FGAVVTLGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,728
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                          SHVAISAPVSAQPVDASVGLAW--LAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGV
                                                             AVSIIVSGTNFIFTLVAFFSIDKIGRRTILLIGLPGMTMALVVCSIAFHF-
                                                                                       LASVVVGVIQVLFTAVAALIMDRAGRR--LLLVLSGVVMVFSTSAFGAYFKLTQGGPGNS
                                                                                                                                                                                                                                                 {\tt APLFISEIAPKMIRGRLTVINSLWLTGGQLVAYGCGAGLNYVNNGWRILVGLSLIPTAVQ}
                                                                                                                                                                                                                                                                               APVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE-----WRWLAVLGCVPPSLM 172
-LGIKFDGAVAVVVSSGFSSWGIVIIVFIIVFAAFYALGIGTVPW-QQSELFPQNVRGI
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Lamsa, Michael
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                                                                                                                                                   ---PGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSS 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 518.5; DB 2;
Pred. No. 4.7e-42;
31; Mismatches 200;
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US-09-031-392-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5942398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
202 -WGSEQG----WEDPPIGAEQSFHLALLROPGI----YKPFIIGVSLMAFQQLSGVNAVMF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                          191 G--LESLLGTASLWPLLLGLTVLPALLQLVLLPFCPESPRYLYIIQNLEGPARKSLKRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                      153 GWVLE------WRWLAVLGCVPPSLMLLLMCFMPETPRFL-LTQHRRQEA-IALRFL- 201
                                                                                                    131 AAASYEMLILGRELIGAYSGLTSGLVPMYVGEIAPTHLRGALGTLNQLAIVIGILIAQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tartagli
APPLICANT: Weng, Xu
TITLE OF INVENTION:
                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                            5 LAAFAAALGPLSFGFA----
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meiklejohn, Ph.D., An REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 GTSYATATNWAGSLVIASTFLTMLQNITPAGTFAFFAGLSCLSTIFCYFCYPELSGLELE 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                               AAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLA 152
                                                                                                                                                               ----GTLTTLWALSVAIFSVGGMISSFLIGIISQWLGRKRAMLVNNVLAVLGGSLMGLAN 130
                                                                                                                                                                                                   ASWFGAVVTLGA---
                                                                                                                                                                                                                         LAVFSAVLGSLQFGYNIGVINAPQKVIEQSYNETWLGRQGPEGPS----SIPP------
                                                                                                                                                                                                                                                                                             155;
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                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            509 amino acids amino acid
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                                                                                                                                                                                   ENCODING GLUTEX
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                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                     Score 516; DB 2;
Pred. No. 6.7e-42;
33; Mismatches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07334/072001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
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                                                                                                                                                                                                                                                     -LGYSSPAIPSLQRAAPPAPRLDDAA 45
                                                                                                                                                                                                                                                                                        163;
                                                                                                                                                                                                                                                                                                                 Length 509,
                                                                                                                                                                                                                                                                                   Indels 102;
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US-09-299-549-6
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                                                                                                              Matches
                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-APR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tarta
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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SOFTWARE: FastSE
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46 ASWFGAVVTLGA------AAGGVLGGWLV----DRAGRKLSLLLCSVPFVAG---FAV1T 92
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                                                                          LAAFAAALGPLSFGFA----
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                                     LAVFSAVLGSLQFGYNIGVINAPQKVIEQSYNETWLGRQGPEGPS---SIPP-----
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                                                                                                            83;
                                                                                                                           Score 516; DB 4;
Pred. No. 6.7e-42;
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                                                                                                            Mismatches
                                                                      -LGYSSPAIPSLORAAPPAPRLDDAA 45
                                                                                                            163; Indels 102;
                                                                                                                                            Length 509;
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                                                                                       TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods for MOTIFIED OF INVENTION: a Polypeptide
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                                                                                         TELEPHONE: 212-878-9655
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SOFTWARE: FASTSEC
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                  STRANDEDNESS:
                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                NAME: Lambiris, Elias REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                     CLASSIFICATION:
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US-08-355-844-3
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Best Local Similarity 28.0
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 CGPYVFFLFAGVLLAFT-LFTFFKVPETKGKSFEEIAAEFQ 500
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                                                                                                                           COUNTRY: USA
ZIP: 10112-0228
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                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             COMPUTER:
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FILING DATE:
                                                                                                                                                              STATE:
                                                                                                                                                                                    ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
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             APPLICATION NUMBER:
                                                                                                                                                                          CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP----RLDDAAAS------WFGAV--VTLGAAAGGVLGGWLVDRAGRKLSLLLCSV----82
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                                                                                                                                                           ΝΥ
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                                                                                                                                                                                                                                                                                                       Li, Jun
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 14-DEC-1994
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28.0%;
          US/08/355,844
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Pred. No. 1e-40;
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 444
                               433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                     391 VAELESQGPRPAAIAVAGFSNWTSNFIVGMCFQYVEQLCGPY
                                                                                          373
                                                                                                                        340
                                                                                                                                           313 GAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLL 372
                                                                                                                                                                                 292
                                                                                                                                                                                                            253
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..492
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Tang, Henry Y.S
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RVFLAAFAAALGPLSFGFALG-----
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 FFIRTYFKVPETKGRTFDEIASGF
               FC-----VPETKGKTLEQITAHF
                                                                                                                                                                                            G--LDSIMGNKDLWPLLLSIIFIPALLQCIVIPFCPESPRFLLI-NRNEENRAKSVLKKL 231
                                                                                                                                                                                                                                                               WGSEQGWEDPPIGAEQSFH------LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVM 252
                                                                                                                                                                                                                                                                                                                                                                                                                                             DDAAASWFGAVVTLGAAAGGVLG----GWLVDRAGRKLSLLLCS-VPFVA----GFAVIT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPT------ 59
                                                                                    \tt MSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTL
                                                                                                                -------GLAGMAGQAILMTIALALLEQLPWMSYLSIVAIFGFVAFFEVGPGPIPWFI
                                                                                                                                                                            YYSTSIFEKAGVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLI----
                                                                                                                                                                                                                                    RGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVF
                                                                                                                                                                                                                                                                                                                        GWVLE-----WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAIA---LRFL 201
                                                                                                                                                                                                                                                                                                                                                        -GKSFEMLILGRFIIGVYCGLTTGFVPMYVGEVSPTAFRGALGTLHQLGIVVGILIAQVF 174
                                                                                                                                                                                                                                                                                                                                                                                    AAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLA 152
                                                                                                                                                                                                                                                                                                                                                                                                                 -TLTTLWSLSVAIF--SVGGMIGSFSVGLFVNRFGRRNSMLMMNLLAFVSAVLMGFSKL- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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212-765-2519
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Pred. No.
4.67
                            450
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                                                         -VFIIFTVLLVL
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15;

RESULT 10
PCT-US95-16126-3
; Sequence 3, Application PC/TUS9516126
; GENERAL INFORMATION:

390

312 291

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APPLICANT: APPLICANT:

Czegledy, Iserovich, Fischbarg,

Jorge

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,408-2586
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cheung, Min TITLE OF INVENTION: A N TITLE OF INVENTION: STH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1.492
OTHER INFORMATION:
OTHER INFORMATION:
   253
                                                                                                                                                                                     116
                                                                     202 WGSEQGWEDPPIGAEQSFH------LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVM 252
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TO NO:
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CITY: New York
                                                                                                                                                                                                                   93 AAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGTLLAYLA 152
                                                                                                                                                                                                                                                                                                                                11 RLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 492 amino acids
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FYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAF 312
                                     RGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVF
                                                                                                           G--LDSIMGNKDLWPLLLSIIFIPALLQCIVIPFCPESPRFLLI-NRNEENRAKSVLKKL 231
                                                                                                                                               GWVLE-----WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAIA---LRFL 201
                                                                                                                                                                                                                                                                                                                                                                  DDAAASWFGAVVTLGAAAGGVLG----GWLVDRAGRKLSLLLCS-VPFVA----GFAVIT 92
                                                                                                                                                                                 -GKSFEMLILGRFIIGVYCGLTTGFVPMYVGEVSPTAFRGALGTLHQLGIVVGILIAQVF 174
                                                                                                                                                                                                                                                         -TLTTLWSLSVAIF--SVGGMIGSFSVGLFVNRFGRRNSMLMMNLLAFVSAVLMGFSKL- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 492; DB 5; 28.8%; Pred. No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Facilitative glucose transportor Glut1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/355,844
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US-09-031-392-4
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                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                    Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MelKlejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tartaglia APPLICANT: Weng, Xun
139 AMLVVNVLSIAGNLLMGLAKMGPSHILIIAGRAITGLYCGLSSGLVPMYVSEVSPTALRG 198
                                                                                                                                                                                                                                                                                                                                                                   TYPE: am TOPOLOGY:
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                                                                                                                                                                                                                                Local Similarity hes 149; Conser
                      76 SILLCSVPFVAGFAVITAAQ---DVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRG 132
                                                                          79 TEAWGSSEGTLAPSAGFEDPTVSPHILTMYWSLSVSMFAVGGMVSSFTVGWIGDRLGRVK 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                        5 LAAFAAALGPLSFGFALG-YSSP-----AIPSLQRAA----
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                                                                                                                                                    LSVFTAVLGFFQYGYSLGVINAPQKVIEAHYGRMLGAIPMVRHATNTSRDNATITVTIPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFIRTYFKVPETKGRTFDEIASGF 467
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                                                                                                            -----GLAGMAGQAILMTIALALLEQLPWMSYLSIVAIFGFVAFFEVGPGPIPWFI 390
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                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                       534 amino acids
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                            20.7%; Score 480; DB 2;
28.0%; Pred. No. 2.2e-38;
Live 91; Mismatches 168
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US-09-299-549-4
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US-09-299-549-4
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Query Match
Best Local
                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                        REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                              MOLECULE TYPE:
                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tartac
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No. 2.2e-38;
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                     APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for M
TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                              CITY:
STATE:
FILING DATE: 1:
CLASSIFICATION:
                                                                              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                               COUNTRY:
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                                 APPLICATION NUMBER:
                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                              New York
                                                                                                                                                                                                          405 Lexington Avenue
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                12-SEPT-1997
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ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J

NAME: Lambiris, Elias J REGISTRATION NUMBER: 33

33,728

4944.200-US

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09031392 Patent No. 5942398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.1%; Score 466.5; DE Best Local Similarity 30.2%; Pred. No. 4e-37; Matches 147; Conservative 81; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID MOLECULES
THEREOF
                                                                                                                                                                                                                                                                APPLICANT: Tarta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 MLLLMCFMPETPRFLLTQHRRQEA-IALRFLWGSE-----QGWE----DPPIGAEQS 218
                                                                     COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                      467 PETKGK 472
COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95
                                                                                                                STATE:
                                                                                                                                STREET: 225 | CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGPEAVGAAQSWALGANWIATFIVAQFFPMLNDLLGGRGKIYWIFAAMACLLGSFIYWWV 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGP1PWLLMSEI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGPIYISEIAPPSAKGLFGAFTQIMTNVGILLTQSLGYFLSKGSMWRVILAIAGAI-GCL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITTLGPLQFGYHLAELNAPQAVITCERKSIHSTTTRGLPQCIPMNPSQFGLVSSIYTLG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYG-AFWLASAFCIFSVLFTLFCV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQTILPTTAALLSVIISAINLVITLACSPLPDKIGRRSCLLLSISGMGLNSVLLALAIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRR--LLLVLSGVVMVFSTSAFGAYF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LLSPPSGNMPPKQPPVTMMRAITDSFYRPAIIAVVGVMVSQQFTGVNSIIMYSVSL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLGLFLVPESPIWLADHQKGNVARQVLQRIRGRDADIEPEVEGWRTSAAPEHSSGEEQS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLGALLAGPVSTKHGRLFTLRATTIFFILGPIAETFAPSIPVLSMGRLLSGVGAGASIV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAAALGPLSFGFALG-YSSP-AIPSLQRAAPPA-----PRLDDAAASWFG---AVVTLG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                  225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ALSA-----IAV---LLFVASFAAGLGPVPFILASEL 406
                                                                                                                                                                                                                                                                                  Tartaglia, Louis A.
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US-09-299-549-3
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                                                                                                                                                                                                                                                               Sequence 3, Application US/09299549 Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tartag
APPLICANT: Weng,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 383 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: 05/09/031,392
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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TELEFAX: bi.,
TEX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                          288 QGPRPAAIAVAGESNWTSNFIVGMCFQYVEQLCGPY------VFIIFTVLLVLEFIFTY 340
                                    COUNTRY: USA
ZIP: 02110-2804
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                                                                     STATE:
                                                                                                      ADDRESSEE: Fish & Ric
STREET: 225 Franklin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 MLILGRFIIGVYCGLTTGFVPMYVGEVSPTELRGALGTLHQLGIVVGILIAQVFG·-LDS
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                                                                                                                                                                                                                                                                                                                                                                     FKVPETKGRTFDEIASGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVL-----FTL 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GLAGMAGCAVLMTIALALLEQLPWMSYLSIVAIFGFVAFFEVGPGPIPWFIVAELFS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----wrwlavlgcvppslmlllmcfmpetprflltqhrrqeaia---lrflwgseqg 207
                                                                                       Boston
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                                                                                                                                                                         NUCLEIC ACID MOLECULES ENCODING GLUTEX AND USES THEREOF
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                                                                                                                      Richardson P.C
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Search completed: February 13, 2002, 21:51:37 Job time: 6264 sec
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TELEX: 200154
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENCTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,544
FILING DATE: 26-APP-1000
PRIOR ADDITO: 26-APP-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.3%; Score 447.5; DB 4; Length 383; Best Local Similarity 31.0%; Pred. No. 2e-35; Matches 117; Conservative 73; Mismatches 131; Indels 57
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APPLICATION NUMBER: 09/031,392

FILING DATE: 26-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/072002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-8906

TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                   433 FCVPETKGKTLEQITAHF 450
                                                                                                                                    341 FKVPETKGRTFDEIASGF 358
                                                                                                                                                                                                                                     288 QGPRPAAIAVAGFSNWTSNFIVGMCFQYVEQLCGPY-----VFIIFTVLLVLFFIFTY 340
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                                                                                                                                                                                                                                                                                                                                                 ---GLAGMAGCAVLMTIALALLEQLPWMSYLSIVAIFGFVAFFEVGPGPIPWFIVAELFS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEKAGVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLI---
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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2324
1 RRVFLAAFAAALGPLSFGFA.....CVPETKGKTLEQITAHFEGR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 13, 2002, 20:10:58; Search time 79.58 Seconds (without alignments) 433.615 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                      219241
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

23	2 0	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	σ	υτ	4	ω	2	1	Result No.
0.20	7 0	529	530.5	532.5	534	534.5	535	535.5	535.5	536	542	545	550	555.5	565	566	569	572	574	577.5	589	589	589	593	596	601.5	717.5	725.5	Score
22.0	۸ د	22.8	2.	2.	ω.	ω.	ω.	ω.	w ·	w ·	ω ·	u ·	ω.	w ·		٠		24.6	4	4.	5.	5	5.	5	5	5	30.9	31.2	Query Match I
307	495	468	534	523	526	523	522	491	491	461	560	464	457	580	496	493	493	496	575	521	472	472	464	464	472	461	490	487	Length E
٨	) K	N	2									Ν							N				2	N	2	N	N	2	DB
101844	A41264	S10014	S38435	S06920	T01853	S25015	A31556	в86096	A26430	G85059	T51485	F69587	E70070	D86426	A31986	A41751	S38981	T52132	T43400	G84864	E85936	B26430	F85951	F65079	S47089	D70073	T14545	E96782	ID
probable sugar cra	transpo	glucose transport	hexose transport p	glucose transport	probable hexose tr		glucose transport		xylose transport p	probable sugar tra	$\sigma$	L-arabinose transp	metabolite transpo	hypothetical prote	glucose transporte	glucose transport	$\overline{}$	probable sugar tra	myo-inositol trans			L-arabinose isomer	galactose-proton s	galactose-proton s		metabolite transpo	probable sugar tra	l pro	Description

4.4 4.5	43	42	41	A (	ب 9	38	37	36	35	ω 4	3	32	ω 1	30
511 509	512.5	513	514.5	21.	517	517	518.5	519.5	520.5	521.5	521.5	523.5	523.5	523.5
22.0 21.9	22.1	22.1	22.1	٥ ١ ١	22.2	22.2	22.3	22.4	22.4	22.4	22.4	22.5	22.5	22.5
557 492	523	492	508	500	534	509	584	547	522	612	516	522	514	457
22	Ν	2 1	N	J ا	N	Ν	2	N	2	Ν	N	N	Ν	N
T38125 I45902	T10122	\$09705	T05156	108554	S14144	A32101	£69555	C84593	S12042	B40538	T12199	E86246	S25009	н85059
myo-inositol trans glucose transporte	hexose transport p	qlucose transport	probable glucose t	muscle-fat dinose	hexose transport p	glucose transport	myo-inositol trans	probable sugar tra	glucose transport	myo·inositol trans	monosaccharid tran	glucose transporte	monosaccharide tra	probable sugar tra

## ALIGNMENTS

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probable sugar transporter protein - beet (.Species: Beta vulgaris (beet) (.Species: Beta vulgaris (beet) (.Species: Beta vulgaris (beet) (.Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 (.Accession: T14545 (.R. Plant Physiol. 110, 511-52), 1996 (.R. Plant Phys
                   metabolite
                                                                                                                                                                                                                                        QΥ
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                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                              дb.
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Best Local Similarity
                                                                                                                                                            446 MLSWNSGGTESIYMVVCAFTVAFVVIWVPETKGRTLEEIQWSF
                                                                                                                                                                                                                    408 MEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF 450
                                                                                                                                                                                                                                                                                                                                                                                                                                  341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                              WLAVGSMCLFIAGEAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSL 407
                                                                                                                                                                                                                                                                                                                                                                                                              LVDKSGRRLLLIVSSSGMTLSLLVVAMSFFLKEMVSDESTWYSV------FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLA
                                                                                                                                                                                                                                                                                   ILSVVGVVAMVVTFSLGIGAIPWIIMSEILPINIKGLAGSIATLANWFVAWIVTMT-ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYWLPLMIGNGLLILQQLSGINGVLFYSSTIFKEAGVTSSNAATFGLGAVQVIATVVTTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRWLAKMGMMEEFEVSLQVLRGF-----DTDISLEVNEIKRSVASSSKRTTIRFAELRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRFLLTQHRRQE-AIALRFLWGSEQGWEDPPIGAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEIAPONLRGALGSVNQLSVTIGIMLSYMLGLEVPWRILAVLGILPCTILIPGLEFIPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEIAYPAVRGLIGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSHMLLLMCEMPET 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGQISEYIGRKGSLMIAAIPNIIGWLAISFAKDSSFLYMGRMLEGFGVGIISYTVPVYI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLACVLIVALGPIQFGFTAGYSSPT----QSAITNELGLSVAEYSWFGSLSNVGAMVGAI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV 62
      transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVVGVVAMVVFFSLGMGPIPWLIMSEILPVNIKGLAGSIATLANWFFSWLITMT-ANLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGSMCLFIAGEAVGMGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLME 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.9%; Score 717.5; DB 2; 36.1%; Pred. No. 8.7e-47;
   homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82;
   yxcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 175;
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----FVSPDS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Species: Ducing (C;Date: 05-Dec-1997 )
C;Accession: D70073
C;Accession: Oqasawa
               Ъ
                                                         Qy
                                                                                                              DЬ
                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                            Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau V., Golawar, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya akuthors: Yoshikawa, H.; Zumannoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Authors: Yoshikawa, H.; Zumstein, B.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
A; Status: preliminary; nucleic acid sequence not shown: translation not shown A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: yxcC
C;Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-461 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16017.1; PID:g26365
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Bacillus subtilis
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                297
                                                                                                                                                                                                                                               285 AALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVATSAPVSAQPVDASV 344
                                                                                                                                                                                                                                                                                                                                                                 227
                                                                                                                                                                                                                                                                                                                                                                                                                   182
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PLMLSAMGIAWVFMVFSVICLLSFFFAFYMVPETKGKSLEEIEASLKKR
                                                                                                                                 GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEF 404
                                                                                                                                                                                                                                                                                                 KWIRPMLLIGVGLAIFQQAVGINTVIYYAPTIFTKAGLGTSASALGTMGIGILNVIMCIT 296
                                            SSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR 453
                                                                                              STAWMTVVFLGVYTVFYQATWGPVVWVLMPELFPSKARGAATGFTTLVLSAANLIVSLVF
                                                                                                                                                                                                     AMILIDRVGRKKLLIWGSVGITLSLAALSGVL-LTLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                FMPETPRFLLTQHRRQEAIAL------RFLWGSEQGWEDPPIGAEQSFHLALLRQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSEMAPTKIRGTLGTMNNLMIVTGILLAYIVNYLFTPFEAWRWWVGLAAVPAVLLLIGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSGTCSDRWGRRKVVFVLSIIFIIGALACAFSQTIGMLIASRVILGLAVGGSTALVPVY
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                                                                                                                                                                                                                                                                                                                                                 PGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF--KDSSLASVVVGVIQVLFTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVY 121
                                                                                                                                                                                                                                                                                                                                                                                                        FMPESPRWLVKRGSEEEARRIMNITHDPKDIEMELAEMKQGEAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKYMIYFFGALGGLLYGYDTGVISGALLFINNDIPLTTLTEGLVVS----MLLLGAIFGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 601.5; DB 2
Pred. No. 4.6e-38;
95; Mismatches 191
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                                                                                                                                                                                                  AST----
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arabinose-proton symporter - Klebsiella oxytoca C:Species: Klebsiella oxytoca C:Date: 13.Jan-1995 #sequence_revision 13-Jan-1995 #text_change C:Accession: S47089

24-Sep-1999

RESULT S47089

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A; Gene:
C; Superf
                                                                                                                                                                                                             galactose-proton symport (galactose transporter) - Escherichia coli (strain C:Species: Escherichia coli C:Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 24-Sep-1999 C:Accession: F65079
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: F65079
                                                                                                A;Cross-references: GB:AE000377; GB:U00096; NID:q2367178; A:Experimental source: strain K-12, substrain MG1655 C;Genetics:
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A; Cross-references: EMBL:X79598;
C:Superfamily: 9lucose transport
C; Keywords: arabinose transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Shatwell, K.P.; Charalambous, B.M.; McDonald, T.P.; Henderson, P.J.F. submitted to the EMBL Data Library, June 1994
A:Description: The nucleotide sequence of the gene araE for arabinose-proton
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A; Accession: S47089
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Nature 409, 529-533, 2001
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                                 EIAYPAVRGLLGSCVQLMVVVGILLAYLA----GWVLEWRWLAVLGCVPPSLMLLLMCFM 179
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ETAPEKIRGSMISMYQLMITIGILGAYLSDTAFSYTGAWRWMLGVIIIPAILLLIGVFFL
                                                                        SGWLSFKLGRKKSLMIGAILFVAGSLFSAAAPNVEVLILSRVLLGLAVGVASYTAPLYLS 131
                                                                                                         GGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYIS 123
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                                                                                                                                                                                                                                          Score 589; DB 2; Pred. No. 4.1e-37;
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3; Mismatches
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`ns 173;
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                                                                                                                                                                                                                                                            Length 464;
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K.; Ap
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A; Map position: 61 min C; Superfamily: glucose C; Keywords: arabinose
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-25, 'Y', 349, 'R' <RES>
A; Cross-references: EMBL: X00072; NID: g40940; PIDN: CAA25075.1; PID: g40941
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
                                                                                                                                                                                    A; Experimental source: strain
C; Genetics:
                                                                                                                                                                                        A;Cross-references: GB:AE000368; GB:U00096; NID:92367165; A:Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-472 <BLAT>
                                                                                                                                                                A; Gene: araE
                                                                                                                                                                                                                                                                                              A:Title: The complete genome sequence of Escherichia coli K-12 A:Reference number: A64720; MUID:97426617 A:Accession: B65067
                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Stoner, C.; Schleif, R.
J. Mol. Biol. 171, 369-381, 1983
A:Title: The araE low affinity L-arabinose transport promoter.
A:Reference number: I40996; MUID:84114868
A:Accession: I40996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: nucleic acid sequence not shown; not compared with conceptual translation A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-472 <MAI>
R:Maiden, M.C.J.; Jones-Mortimer, M.C.; Henderson, P.J.F.
J. Biol. Chem. 263, 8003-8010, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:J03732; NID:g145320; PIDN:AAA23469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-472 <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The cloning, DNA sequence, and overexpression of A:Reference number: A28075; MUID:88228015
A:Accession: A28075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-arabinose isomerase (EC 5.3.1.4) - Escherichia coli C:Species: Escherichia coli C:Species: Escherichia coli C:Date: 05-Oct.1988 #sequence_revision 05-Oct.1988 #text_change 24-Sep-1999 C:Accession: B26430; A26075; I40996; B65067 R:Maiden, M.C.J.; Davis, E.O.; Baldwin, S.A.; Moore, D.C.M.; Henderson, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Mammalian and bacterial sugar transport
A:Reference number: A93389; MUID:87115869
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                                                                                     Superfamily: glucose transport; Keywords: arabinose transport;
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                  Length 472,
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                                                                                                                                                                                                      PIDN:AAC75880.1; PID:g1789207
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121 YISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW--RWLAVLG--CVPPSLMLLLM 176

GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120 RMNMFVSVAAAVAGLLFGLDIGVIAGALPFITDHFVLTSRLQE----WVVSSMMLGAAIG  ${\tt RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG}$ 

ALFNGWLSFRLGRKYSLMAGAILFVLGSIGSAFATSVEMLIAARVVLGIAVGIASYTAPL

YLSEMASENVRGKMISMYQLMVTLGIVLAFLSDTAFSYSGNWRAMLGVLALPAVLLIILV

195

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A;Gene: araE
C;Superfamily:
                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005174; NID:g12517333; PIDN:AAG57953.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-472 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein araE [imported] - Escherichia coli (strain 0157:H7) (; Species: Escherichia coli (c. Species: Escheria) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Grotbeck, E.J.
19, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLPNSPRWLAEKGRHIEAEEVLRMLRDTSEKAREELNEIRESLKLKQGGWALFKINRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFMPETPRFLLTQHRRQEA-IALRFLWGSEQGWEDPPIGAEQSFHL-----ALLR-QPGI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALFNGWLSFRLGRKYSLMAGATLFVLGSIGSAFATSVEMLIAARVVLGIAVGIASYTAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLGGWLVDRAGRKLSLLLCSVÞFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMNMFVSVAAAVAGLLFGLDIGVIAGALPFITDHFVLTSRLQE----WVVSSMMLGAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154;
                                                                                                                                                                                   glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                  25.3%; Score 589; DB 2; 33.5%; Pred. No. 4 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.D.; Rose,
Potamousis,
                                                                                                                                                                                                                                                                                                      GSPDB:GN00145; UWGP
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A:Gene: At2g43330
A:Map position: 2
C:Superfamily: glucose transport protein
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A:Residues: 1-521 <STO>
A:Cross-references: GB:C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A84420; MUID:20083487 A;Accession: G84864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; oo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L. D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, e 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418
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    337
                                                                                                                                 275 YLDVFRSKELRLAFLAGAGLQAFQQFTGINTVMYYSPTIVQMAGFHSNQLALFLSLIVAA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 FTVDKAGRKPALKIGFSVMALGTLVLG--YCLMQFDNGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AALGPLSFGFALGYSSPAIPSL------QRAAPPAPRLDDAAASWFGAVV"L---GAA 58
                                                                                                                                                         HLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLA---SVVVGV
                                                                                                                                                                                                                                                                     LLMCFMPETPRFLLTQHRRQEAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSS 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF---KDSSLASVVVGVIQVLETAVAA
AQPVDASVG---LAWLAVGSMCLFIAGFAVGWGPIPWLLMSETFPLHVKGVATGICVLTNW
                                                                      ILMLFMPESPRWLFMKNRKAEAIQVLARTYDISRLEDEIDHLSAAE---EEEKQRKRTVG 274
                                                                                                                                                                                                                                                                                                                PVYTAEASPSEVRGGLVSTNVLMTTGGQFLSYLVNSAFTQVPGTWRWMLGVSGVPAVTQF
                                                                                                                                                                                                                                                                                                                                                             PVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVL-----EWRWLAVLGCVPPSLML 173
                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGIGGLLFGYDTGVISGALLYIKDDFEVVKQSSFLQVYNVSSFTSSKLETIVSMALVGAM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLDSIGAAGTFWLYTALNIAFVGITFWLIPETKNVTLEHI 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFMPETPRFLLTQHRRQEA-IALRFLWGSEQGWEDPPIGAEQSFHL----ALLR-QPGI
                                            MNAAGTVVGIYFIDHCGRKKLAL-----
                                                                                                                                                                                                                                                                                                                                                                                                       IGAAAGGWINDYYGRKKATLFADVVFAAGAIVMAAAPDPYVLISGRLLVGLGVGVASVTA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE002093; NID:g2289003; PIDN:AAB64332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.8%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 577.5; DB 2;
Pred. No. 3.4e-36;
5; Mismatches 192;
                                                                                                                                                                                                                                                                     -----ALRFLWGSEQGWEDPPIGAEQSF
                                            -SSLFGVIISL------LILSVSFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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C:Superfamily: maltose transport protein MAL61
C:Keywords: sugar transport; transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 968 h90 R; Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Oct-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z99532; PIDN:CAB16718.1; GSPDB:GN00066; SPDB:SPAC7D4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 290-575 <GEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T39079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z21826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X98622; PIDN: CAA67211.1
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A; Residues: 1-575 < NIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Niederberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T43400; T39079
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                                                                                                                                                                                                                                                                                        FK-ELYFNPSNFRALILACGLQAMQQLSGFNSLMYFSSTIFEVVGFNNPTATGLIIAATN 384
                                                                                                                                                                                                                                                                                                                                                                                  WLPESPRLLVKKERSQEAYNTLARIYPTAHPYEIKTKLYLIQEGVRDPFSGSRWQKIVKT 325
                                                                                                                                                                                                                                                                                                                                                                                                            IAGALADFFGRKPVIAIASIIIIVGSIVQVTAHHLWHMIVGRFVIGWGVGIASLIIPLYL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV 62
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                                                               LMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEIAPSKIRGRLVIIYVLLITAGQVIAYGIDTAFEHVHNGWRWMVGLAMVPAAFQLFILI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SETAYPAVRGLLGSCVQLMVVVGTLLAYLAGWVLE-----WRWLAVLGCVPPSLMLLLMC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWVLAFAAGIGGLLFGYDTGVISGALVVIGTSL-GGHELTNGGKEFITSATSLGALLGGI 145
                                                                                                                                                    AQPVDASVGLAWLAVG--SMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNW 394
                                                                                                                                                                                                   FVFTIVAFGVIDFFGRRILLLLTVWGMIAALIVCAVAFHF-LPKDENGNYT------ 434
                                                                                                                                                                                                                                              VLFTAVAALIMDRAGRRLLLVLS--GVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS 336
                                                                                                                                                                                                                                                                                                                                     FHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQ
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                                                                                                            ----SGQSNAWATVVLISMIVYVASYASGLGNLPW-QQSELFPMSVRGLGTGMSTAVNW
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RESULT 12
$38981

91ucose transport protein 3, neuron-specific - rat
N;Alternate names: glucose transporter
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change C;Accession: $38981
R;Nagamatsu, S; Sawa, H.; Kamada, K.; Nakamichi, Y.; Yoshimoto, FEBS Lett. 334, 289-295, 1993
FEBS Lett. 334, 289-295, 1993
FEBS Lett. 334, 289-295, 1993
A;Title: Neuron-specific glu
A;Reference number: S38981;
A;Accession: S38981
A;Molecule type: mRNA
A;Residues: 1-493 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ERD6
C;Superfamil
C;Keywords:
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A:Molecule type: mRNA
A:Residues: 1-496 <KIY>
A:Cross-references: EMBL:D89051; PIDN:BAA25989.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blochim. Biophys. Acta 1370, 187-191, 1998
A;Title: ERD6, a cDNA clone for an early dehydration-induced
A;Reference number: Z25973; MUID:98213606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1370, A; Title: ERD6, a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession:
R;Kiyosue, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable sugar transporter protein ERD6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-200
C:Accession: T52132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A: Accession: T52132
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                                                                                                                                                                                                                                                                                                                                                                         PIFTCIGV-
                                                                                                                                                                                                                                                                                                                                                                                                PVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                          LVDKMGRRTLLMASCSAMGLSALLLSVSYGFQSFGILPELT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMDRAGRRILLVLSGVVMVFST------SAFGAYFKLTQGGPGNSSHVAISAPVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYAYPLIIGVGLMFLQQLCGSSGVTYYASSLFNKGGF-PSAIGTSVIATIMVPKAMLATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRFLLTQHRRQEA-IALRFLWGSEQGWEDPPIGAEQS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.; Abe, H.; Yamaguchi-Shinozaki, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                 glucose transporter (NSGT): CNS distribution of GLUT3 rat B1; MUID: 94063043
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                                                                                                                                                                                                                                                                                                                                                              -HIVSFAMGMGGLPWIIMAEIFPMNVKVSAGTLVTVTNWLFGW 440
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Pred. No. 8.3e-36;
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                                                                                                                                             20-Jun-2000
                                                                                                         K.; Hoshino,
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C;Superfamily: glucose transport protein C;Keywords: glycoprotein; transmembrane protein F;43/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                         glucose transport protein 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-S
C;Accession: A41751; S18128
R;Nagamatsu, S.; Kornhauser, J.M.; Burant,
J. Biol. Chem. 267, 467-472, 1992
A;Title: Glucose transporter expression in
                                                                             C; Genetics:
                                                                                                            A; Molecule type: mRNA
A; Residues: 1-493 < NAG>
                                                             A; Gene:
                                                                                        A;Cross-references: GB:X61093; NID:g51088; PIDN:CAA43406.1;
                                                                                                                                                A;Reference number: A41751; MUID:92112695
A;Accession: A41751
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                                                             GLUT3
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                                                                                                                                                                                               brain.
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L.4e-35;
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   #status
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Query Match Best Local Similarity Matches 153;

24.4%;

Conservative

86;

Score 566; DB Pred. No. 2.3e 86; Mismatches

DB 2;

Length 493;

Indels

74;

Gaps

13;

b

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Cross-references: GDB:11996; Map position: 12p13.3-12p13.3 Superfamily: glucose transport Keywords: muscle: skeletal mus Query Match Best Local Similarity 31.4%; Matches 151; Conservative 3 VFLAAFAALGPLSFGFALGYS :                 10 LIFAITVATIGSFQFGYNTGVI 53 VTLGAAAGGVLGGWLVDRAGRK :                   70 FSVGGMIGSFSVGLFVNRFGRR   110 ACGVASLVAPVYISEIAYPAVR	La Fila Da Da Da La Da La Da	325 341 385 401 445	122 158 182 208 242 265 302	6 13 47 64
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GDB:119996; OMIM: 13.3.12p13.3 SSE transport prot skeletal muscle; Skeletal muscle; 14.3%; Sco rity 31.4%; Pre nservative 88; LGPLSFGFALGYSSPAIP	in, revi dy, 8, 1 of ID:8	GLAWL::::AMSFV	IGEVS MCFMP: :     LPFCP: ROPGIT     RSPNY AALIM: ::: SLFLV	PAIPS LVDRA
ferences: GDB:J19996; OMIM:13817 tion: 12p13.3-12p13.3 ily: glucose transport protein : muscle: skeletal muscle: trans tch al Similarity 31.4%; pred. No 151; Conservative 88; Misma vFLAAFAAALGPLSFGFALGYSSPAIPSLOR- :	In, skeletal revision 21-M revision 21-M s, R.L.; Fan s, 1988 of human glu (D:89008414 NID:9183684;	AVGSMC :::CIVAIL VLRPYG       YLGAY-	VSPTALRGA MPETPRELL   :       CPESPRELL GIYKPFIIG : :  NYVQPLLIS NYVQPLLIS IMDRAGRRL :::	AAFAAALGPLSFGFALGYSSPAIPSLQRAAPPA
protein le: transmembrane Score 565: DB 2 Pred. No. 2.8e-3: 18; Mismatches 1: 18; Mismatches 1: 14PEKIIKEFINKTLTDKG SSLLLCSVPFVAGFA' 1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1:: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1:: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1:: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1::: 1   1:::	skeletal muscle sion 21-May-1990 R.L.; Fan, Y.S.; 988 human glucose tr 9008414 :g183684; PIDN:A	ILFIAG ::::  AIYVAF BAFWLA   : VFIIF	LGRLLIGIFCGLCTGFVPMYİĞEVSPTALRĞAFĞTLN WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTOHRR   :    :      :	AAFAAALGPLSFGFALGYSSPAIPSLORAAPPA
ne ne 2 -3 -3 -3 -1 LA		NSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGV : :: :	-> C	AAFAAALGPLSFGFALGYSSPAIPSLQRAAPPA
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protein  ; Length 496; 5; 1ndels 52; G, 90; Indels 52; G, 11: 1	ige 24-Sep 3.: Shows, 1.ike prote	MSEIFPLHVK :::::  ::  VAELFSOGPR .FCVPETKGKT !                ! FKVPETKGRT	DFILG  DVVQEI  FIFEEA  FIFEEA  FIFEDA  CLTQGG	PRLDDAAA 
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	and			
Oue Bes Mat Oy Oy Db Oy Db	Nature A; Author C: A.; Rizeo A; Author A; Author A; Author A; Author A; Refie A; Resia A; Resia A; Cros C; Genn A; Map	RESULT RESULT D86426 hypoth C; Spec C; Date C; Acce C; Acce Chin,	04 00 00 00 00 00 00 00 00 00 00 00 00 0	ДЬ Ду ДЬ Ду
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Score 555.5; pred. No. 1.7/ 94; Mismatches SpalpSLORAAPPAP;     : :: SGALLYIR SGALLYIR ILLLCSVPFVAGFAVI : :   :   :   :   : : :     :   :   : : :       :   :	Johns S.X. kano, J.R.; Veni omosor 6719	rted] e-ear n 02- .J.; i	LSGVVI : I GFAVGI   :     :   FFEIGI ASAFC: :   FTGFL:	LNQLG: RRQEA: : :   :KEEEN/ MAFQQI
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Length 580; Indels 99SWFGAVV-	os, J.  wick, R.W. Arab	balian hange Kaul	GLGGM GLGGM KGVAT :   RPAAM TLEQI	GSEEL DPPIGA DIQEMK CAKFKD   ::
	te 408, 816-820, 2000 hors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, Y. M.; Rooney, T.; Rowley, D.; Sakano, H. hors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. Le: Sequence and analysis of chromosome 1 of the plant Arabidopsis. erence number: A86141; MUID:21016719 ession: D86426 tus: preliminary ecule type; DNA idues: 1-580 <570> ss-references: GB:AE005172; NID:g11120774; PIDN:AAG30955.1; GSPDB:GN00 ss-references: GB:AE005172; NID:g11120774; PIDN:AAG30955.1; GSPDB:GN00 position: 1	468 Q 468  7 15  6 cies: Arabidopsis thaliana (mouse-ear cress) cies: Arabidopsis thaliana (mouse-ear cress) cies: Arabidopsis thaliana (mouse-ear cress) cies: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 ession: D86426 cies: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H., N.F.; Hughes, B.; Huizar, L.	VVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAIS      :	FCGLCTGFVPMYIGEISPTALRGAFGTLNQLGIVVGILVAQIFGLEFILGSEELWPLLLGCVPPSLMLLLMCFMPETPRFLLTOHRRQEAIALRFLWGSEQGWEDPPIGAEQSFH-
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	, Kim, Marzia Tallo	Alon ar,		

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LALLROPGTYKPFTIGVSLMAFQOLSGVNAVMFYAETIFEEAKFKDSSLASV :   :

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pfam; pF00083; sugar_tr; 1.
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                                                       STRAIN-8017
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARABINOSE-PROTON SYMPORTER (ARABINOSE TRANSPORTER).
                                                                                                                    NCBI_TaxID=571;
                                                                                                                                          Klebsiella
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVL----EWRWLAVLGCVPPSLMLLLMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALSGTCSDRWGRRKYVFYLSIIFIIGALACAFSQTIGMLIASRVILGLAVGGSTALVPVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150;
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SUGAR_TRANSPORT_2; 1.
embrane; Complete prot
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50235 MW;
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31.8%;
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Pred. No. 1.2e-33;
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  McDonald T.P.,
                                                                                                                                                                                                                                                                                                                    472 AA
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Henderson
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Best Local :
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PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, sequencing, and expression of the araE gene of Klebsiella Oxytoca 8017, which encodes arabinose-H+ symport activity.";
J. Bacteriol. 177:5379-5380(1995).
-! FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                7 AFAAALGELSEGFALGYSSPAIPSLQRAAPPAPRLDDAAASWEGAVVTLGAAAGGVLGGW 66
MTMMCIAGYAMSAAPVVWILCSEIQPLKCRDFGITCSTTTNWVSNMIIGATE
                                                                              GRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVG
                          SMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLM
                                                           GRKPALKIGFSVMAIGTLVLG--YCLMQFDNGT
                                                                                                            GMLLQAMQQFTGMNIIMYYAPRIFKMAGFTTTEQQMVATLVVGLTFMFATFIAVFTVDKA
                                                                                                                                       GVSLMAFQQLSGVNAVMFYAETIFEEAKF---KDSSLASVVVGVTQVLFTAVAALIMDRA
                                                                                                                                                                   PRWLAEKGRHVEAEEVLRMLRDTSEKARDELNEIRESLKLKQGGWALFKVNRNVRRAVFL\\
                                                                                                                                                                                              PRFLLTQHRRQEA-IALRFLWGSEQGWEDPPIGAEQSFHL-----ALLR-QPGIYKPFII
                                                                                                                                                                                                                          SENVRGKMISMYQLMVTLGIVMAFLSDTAFSYSGNWRAMLGVLALPAVVLIILVIFLPNS
                                                                                                                                                                                                                                                     YPAVRGLLGSCYQLMVVVGILLAYLAGWVLEW--RWLAVLG--CVPPSLMLLLMCFMPET
                                                                                                                                                                                                                                                                                  LSFRLGRKYSLMVGAVLFVAGSVGSAFATSVEMLLVARIVLGVAVGIASYTAPLYLSEMA
                                                                                                                                                                                                                                                                                                           LVDRAGRKLSLLLCSVPFVAGFAVITAAQDVMMLLGGRLLTGLACGVASLVAPVYISEIA 126
                                                                                                                                                                                                                                                                                                                                      SIAAAVAGLLFGLDIGVIAGALPFITDHFVLSSRLQE----WVVSSMMLGAAIGALFNGW 81
                                                                                                                                                                                                                                                                                                                                                                                                         153;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugar transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 596; DB 1;
Pred. No. 8.3e-33;
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; 410021E1BEE3D96E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane; Symport
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 472;
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                                                       ASSGLSWLSV
                                                                                                                                                                                                                                                                                                                                                                                              36;
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413 PYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI

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GALP_ECOLI
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                    Query Match
Best Local Similarity
Matches 156; Conser
                                                                                                                                                                                                                                                     TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALP_ECOLI STANDARD: PRT: 464 AA. p37021; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GALACTOSE-PROTON SYMPORTER (GALACTOSE TRANSPORTER).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-i- FUNCTION: UPTAKE OF GALACTOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003663; Sugar_trnsportr
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                        PS00217; SUGAR_TRA
t; Sugar transport;
                                                                                                                                                                                                                                                                                                                                                                                                        PS00216; SUGAR_TRANSPORT_1; 1. PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                      proteome.
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                        83;
                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                    Score 593; DB 1;
Pred. No. 1.3e-32;
3; Mismatches 173
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Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                          Inner membrane;
                        173;
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                                                        Length 464
                        Indels
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thew G.F.,
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P09830; Q46937;
01-MAR-1989 (Rel. 1
01-MAR-1989 (Rel. 1
20-AUG-2001 (Rel. 4
                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., Ro
Gregor J., Davis N.W., Kirkpatrick H.A., Go
                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                             maiden M.C.J., Jones-Mortimer M.C., Henderson P.J.F.; "The cloning, DNA sequence, and overexpression of the coding for arabinose-proton symport in Escherichia co J. Biol. Chem. 263:8003-8010(1988).
                                                                                                                                                                                                                                                                                                                                                "Mammalian and bacterial sugar transport Nature 325:641\cdot643(1987).
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ARABINOSE-PROTON SYMPORTER (ARABINOSE TRANSPORTER).
ARAE OR B2841 OR Z4161 OR ECS3698.
                    "The complete genome sequence of Science 277:1453-1474(1997).
                                                          Mau B.,
                                                                                                                                                                                                                                                                     MEDLINE=88228015; PubMed=2836407;
Maiden M.C.J., Jones-Mortimer M.C.,
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / JM243
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Henderson P.J.F.;
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                                                            Shao Y.;
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                                        Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                            S.A.,
                                                                            Goeden M.A., Rose
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ode C.K., Mayhew
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a coli Kl2.";
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                                                                                            Burland V.
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InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; Sub_trnsportr.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
PROTERRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory proteins.";
J. Mol. Biol. 171:369-381(1983).
J. Mol. Biol. 171:369-381(1983).
FUNCTION: UPTAKE OF ARABSINOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANY EXPORT OF A PROTON (SYMPORT SYSTEM).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INVER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156/31; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy, Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 'Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunao Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The araE low affinity L-arabinose transport promoter. Cloning, sequence, transcription start site and DNA binding sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE OF 1-28 FROM N.A. MEDLINE-84114868; Pubmed=6319708; Stoner C., Schleif R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
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A28075; A28075.
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X00272;
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AE005513; AAG57953.1;
AP002563; BAB37121.1;
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SUGAR_TRANSPORT_2; 1.
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ort; Transmembrane;
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M., Tobe T.,
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Best Local
                             Gentles S., Churcher C.M., Wood V., Barrell B.G., Ra Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databa!- FUNCTION: TRANSPORTER FOR MYO-INOSITOL.
This SWISS-PROT entry
                                                                                                                 MEDLINE-9828265; PubMed-9560432; MEDLINE-9828265; PubMed-9560432; Niederberger C., Graub R., Schweingruber A.-M., Fankhauser H., Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.; "Exogenous inositol and genes responsible for inositol transport are required for mating and sporulation in Shizosaccharomyces pombe."; Curr. Genet. 33:255-261(1998).
                                                                                                                                                                                                                                                                                                                                                       Q10286;
01-NOV-1997
                                                                                        STRAIN=972;
                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=968 H90;
                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schiz
                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel.
MYO-INOSITOL TRANS
ITR1 OR SPAC7D4.01
                                                                                                                                                                                                                                                                                                                                                                                               _SCHPO
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
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Pred. No. 2.4e-32;
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV
AGNLGIGASFLTLMSEITPTGTFALYGGLCFLGWLGALFCYPDLTDYTIEE1
                               LMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI 446
                                                                                            AQPVDASVGLAWLAVG---SMCLFTAGFAVGWGPTPWLLMSEIFPLHVKGVATGICVLTNW
                                                                                                                             FVFTIVAFGVIDFFGRRILLLLTVWGMIAALIVCAVAFHE-LPKDENGNYT
                                                                                                                                                          VLFTAVAALIMDRAGRRLLLVLS--GVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS
                                                                                                                                                                                         FK-ELYENPSNERALILACGLQAMQQLSGENSLMYFSSTIFEVVGENNPTATGLIIAATN
                                                                                                                                                                                                                         FHLALLROPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQ
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                                                                                                                                                                                                                                                                                     FMPETPRFLLTQHRRQEA---IALRF------
                                                                                                                                                                                                                                                                                                                    SEIAPSKIRGRLV1IYVLLITAGQVIAYGIDTAFEHVHNGWRWMVGLAMVPAAFQLFILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00216; SUGAR_TRANSPORT_1; 2.
PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003663; Sugar_trnsportr
                                                               SGQSNAWAIVVLISMIVYVASYASGLGNLPW-QQSELFPMSVRGLGTGMSTAVNW
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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Pred. No. 2.
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9.9e-31;
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                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental gene expression in the placenta."; Placenta 18:393-401(1997).
-!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS0021
PROSITE; PS0021
                                                                                                                                                                                                                                                                                                                                                                                          pfam: PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR01192; GLUCTRSPORT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Currie M.J., Bassett N.S., Gluckman P.D.; "Ovine glucose transporter-1 and -3: cDNA partial sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97392487; PubMed=9250701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 88-248 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Mol. Biol. Int. 37:9-16(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporters."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett B.L., Prosser C.G., Grigor M.R.: "Isolation of cDNAs and tissue specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COOPWORTH;
MEDLINE=96109471; PubMed=8653093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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SEQUENCE
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                                                                                                                                        MEDLINE-94063043; PubMed-8243635; MEDLINE-94063043; PubMed-8243635;
                                                                                                                                                                                                                                                          007647; 062729;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
GLUCOSE TRANSPORTER TYPE 3, BRAIN.
                  STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; MEDLINE-96042338; PubMed=7475896; Krishnan S.N., Haddad G.G.;
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                           GTR3_RAT
                                                              SEQUENCE FROM N.A.
                                                                                                                             Hoshino T
                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                SLC2A3 OR GLUT3 OR GLUT-3.
 "Cloning of glucose transporter-3 Life Sci. 56:1193-1197(1995).
                                                                                                   "Neuron-specific glucose transporter (RGT3)
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                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                             PRT;
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in rat central neurons.";
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                cDNA from rat brain.";
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CONFLICT
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pfam; pF00083; sugar_tr; 1.
pRINTS; pR00171; SUGRTRNSPORT.
pRINTS; pR00172; GLUCTRNSPORT.
pRINTS; PR01192; GLUCTRSPORT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D13962; BAA03065.1; EMBL; U17978; AAA62503.1; PIR; S38981; S38981.
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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QEMKDESIRMSQEKQVTVLELFKSPSYFQPLLISVVLQLSQQFSGINAVFYYSTGIFQDA
                          QGWEDPPIGAEQSFH----LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEA
                                                                                                                                                                                             LLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAG--WVL-
                                                                                                                                                                                                                                       LWSLCVAIFSVGGMIGSFSVGLFVNRFGRRNSMLLVNLIAILGGCLMGFAKI--AESVEM
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                                                                                                                                                        LILGRLIIGIFCGLCTGFVPMY1GEVSPTALRGAFGTLNQLGIVVGILVAQVFGLDFILG
                                                                                                                                                                                                                                                                                                                   AVTVATIGSFQFGYNTGVIN-----APETIIKDFLNYTLEERLEDLPRE--GLLTT
                                                                            SEELWPGLLGLTIIPAILQSAALPFCPESPRFLLINRKEEDQATEILQRLWGTPDVIQEI
                                                                                                                 -EWRWLAVLG--CVPPSLMLLLMCFMPETPRFLLTQHRRQEAIA--LRFLWGSE-----
                                                                                                                                                                                                                                                                                                                                                                                                   153;
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                 91;
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CYMOPLASMIC (POTENTIAL).

N-LINKED (GLCMAC. . .) (I
R -> S (IN REF. 2).
S -> F (IN REF. 2).
H -> Q (IN REF. 2).
H -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 569; DB 1;
Pred. No. 5.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSPORTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                   169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTR3_MOUSE STANDARD; PRT; 493 AA. p32037; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) GLUCOSE TRANSPORTER TYPE 3, BRAIN.
                             EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeda J., Minokoshi Y., Yasuda K., Kayano T., Graeme B Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUT3, the brain facilitative glucose transporter identification of sites of expression by in situ h. Biol. Chem. 267:467-472(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92112695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLC2A3 OR
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A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A41751; A417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \begin{array}{lll} \textbf{SIMILARITY:} & \textbf{HIGH TO OTHER GLUCOSE TRANSPORTERS.} \\ \textbf{SIMILARITY:} & \textbf{BELONGS TO THE SUGAR TRANSPORTER FAMILY} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: HIGHLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a ceen the Swiss institute of Bioinformatics and the EMBL European Bioinformatics institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G.I.
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                                                                                                                                                                                                                                              U11844;
U11845;
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                                                                                                                                                                                                                                                                                                               U11853;
                                                                                                                                                                                                                                                                                                                                               x61093;
                                                                                                                                                                                                                                                                                                                                                                            M75135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter expression in brain. cDNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUT3 OR GLUT-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                      equires a license agreement ( email to license@isb-sib.ch)
                                                                                       AAB60666.1;
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nhauser J.M., Seino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN BRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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InterPro: IPR003662; sub_trnsportr.
Pfam: PF00083; sugar_tr; 1.
PRINTS: PR00171; SUGATRNSPORT.
PRINTS: PR01192; GLUCTRNSPORT.
PRINTS: PR01192; GLUCTRSPORT3.
PROSITE: PS00216; SUGAR_TRANSPORT_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01192; GLUCTRSPORT3.
PROSITE; PS00216; SUGAR_TRANSPORT_1;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
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nes 153; Conservative
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9
                                DIARAFEGQ
                                                     QITAHFEGR
                                                                           AIAVAGCCNWTSNFLVGMLFPSAAAYLGAY-VFIIFAAFLIFFLIFTFFKVPETKGRTFE
                                                                                                                      GMAVCSVFMTISLLLKDDYEAMSFVCIVAILIYVAFFEIGPGPIPWFIVAELFSQGPRPA
                                                                                                                                                                QEPIYATIGAGVVNTIFTVVSLFLVERAGRRTLHMI--
                                                                                                                                                                                     KDSSLASVVVGVTQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPG
                                                                                                                                                                                                        MKDESVRMSQEKQVTVLELFRSPNYVQPLLISIVLQLSQQLSGINAVFYYSTGIFKDAGV
                                                                                                                                                                                                                               WEDPPIGAEQSFH----LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF
                                                                                                                                                                                                                                                     ELWPGLLGLTIIPAILQSAALPFCPESPRFLLINKKEEDQATEILQRLWGTSDVVQEIQE
                                                                                                                                                                                                                                                                         WRWLAVLG -- CVPPSLMLLLMCFMPETPRFLLTQHRRQEAIA -- LRFLWGSE-----QG
                                                                                                                                                                                                                                                                                               LGRLLIGIFCGLCTGFVPMYIGEVSPTALRGAFGTLNQLGIVVGILVAQIFGLDFILGSE
                                                                                                                                                                                                                                                                                                           GGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAG--WVL--E
                                                                                                                                                                                                                                                                                                                                           SLCVAIFSVGGMIGSFSVGLFVNRFGRRNSMLLVNLLAIIAGCLMGFAKI--AESVEMLI 121
                                                                                                                                                                                                                                                                                                                                                     SWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFV-----AGFAVITAAQDVWMLL 101
                                                                                                                                                                                                                                                                                                                                                                                                         AAFAAALGPLSFGFALGYSSPAIPSLQRAAPPA-----PRLDD------AAA
                                                                                                ATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLE
                                                                                                                                           NSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGV
                                                                                                                                                                                                                                                                                                                                                                                    AVTVATIGSFQFGYNTGVIN------APETILKDFLNYTLEERLEDLPSEGLLTALW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugar transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
64
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325
335
387
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                                                                                                                                                                                                                                                                                                                                                                                                                                          24.4%;
31.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 566; DB
Pred. No. 8.5e
86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9090B8DCB8780082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          566; DB 1;
No. 8.5e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                ---GLG
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                      400
                                                                                                                                                                                                                                264
                                                                                                                                           384
                                                                                                                                                                340
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                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                     241
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GTR3_HUMAN
ID GTR3_HUMAN

STANDARD;

PRT;

496 AA

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                              Qy
                                                      Query Match
Best Local S
Matches 151
                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                           TRANSMEM
TRANSMEM
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TRANSMEM
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGATTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR001792; GLUCTRSPORT3.
                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                       Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                           PROSITE; PS00216; SUGAR_TRANSPORT_1; PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M20681; AAB61083.1; PIR; A31986; A31986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCOSE TRANSPORTER.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and gene localization of a protein expressed in fe skeletal muscle and other tissues.";
J. Biol. Chem. 263:15245-15248(1988).
-!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A
          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P11169;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCOSE TRANSPORTER TYPE 3, BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89008414; PubMed=3170580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                         3 VFLAAFAAALGPLSFGFALGYSSPAIPSLQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Evidence for a family of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bell G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kayano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLC2A3 OR GLUT3
LIFAITVATIGSFQFGYNTGVINAPEKIIKEFINKTLTDKGNAPPSEVLLTSLWSLSVAI
                                                      151;
                                                                                                                                                                                                                                                                                                                                                                                                                         138170;
                                                               Similarity
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                                                    Conservative
                                                                                                                                             400
428
                                                                                                                                                                             32
65
94
125
125
1154
1184
205
270
336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                                                                                                                                                                                                                                   Sugar
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64
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114
1145
174
204
2269
2269
2269
235
335
335
387
448
                                                            24.3%;
                                                                                                           53924
                                                                                                                                                                                                                                                                                                                transport; Transport;
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                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eddy R.L.,
                                                   ; 88
                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (GLCNAC. . .) (PO
                                               Score 565; DB
Pred. No. 9.9e
88; Mismatches
                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                  CYTOPLASMIC POTENTIAL.
                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                               EXTRACELLULAR
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                                                       9.9e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                       DB 1;
                                                                                                                                                                                                           (POTENTIAL)
                       ----AAPPAPRLDDAAASWFGAV 52
                                               190;
                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                    Length 496;
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                                               Indels
                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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fetal
                                              52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
                                           Gaps
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 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QУ
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                            EMBL; L35267; AAA51454.1; -
                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                      SLC2A3 OR GLUT3
                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSE TRANSPORTER TYPE 3, BRAIN.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P47842;
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                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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                                          non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAG--WVL--EWRWLAVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata;
Carnivora; Fissipedia; Canidae;
Sugar_trnsportr.
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CARBOHYD
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PRINTS; PR00171; SUGETRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR01192; GLUCTRSPORT3.
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PROSITE; PS00217; SUGAR_TKANSPORT_2; 1.
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31.1%;
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N-LINKED (GLCNAC. . .) (F
09063C013DAE39C3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaillou S., Bor Y.-C., Batt C.A., Postma P., Pouwels P., Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
-i-FUNCTION: UPTAKE OF D-XYLOSE ACROSS THE BOUNDARY MEMBRANE THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00171; S
PROSITE; PS00216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00083; sugar_tr;
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                                                                                                                                                     PAVRGLLGSCVQLMVVVGILLAYL----AGWVLEWRWLAVLGCVPPSLMLLLMCFMPET
                                                                                                                                                                                              VDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAY 127
                                                                                                                                                                                                                                                         FAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWL
                                                                            PRFLVKSGHLDEARHVLDTMNKHDQVAVNKEINDIQESAKIVSGGWSE
                                                                                                                             SDKRGTVSSLFQLMVMTGILLAYITNYSFSGFYTGWRWMLGFAAIPAALLFLGGLILPES
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                                         LLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSS--LASVVVGVIQVL
                                                                                                     PRFLLTQHRRQEA------IALRFLWGSEQ-----
                                                                                                                                                                                SDRFGRRKLLLLSAIIFFVGALGSAFSPEFWTLIISRIILGMAVGAASALIPTYLAELAP
                                                                                                                                                                                                                                                                                    140;
                          -LFGKMVRPSLIIGIGLAIFQQVMGCNTVLYYAPTIFTDVGFGVSAALLAHIGIGIFNVI
                                                                                                                                                                                                                                                                                                Similarity
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(Rel. 38, Last annotation update)
OTON SYMPORTER (D-XYLOSE TRANSPORTER)
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STRAIN=015:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
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MEDLINE=21074935; PubMed=11206551;
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"The cloning and u...
symport in Escherichia coli kiz.
symport Chem. 262:13928-13932(1987).
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STRAIN=0157:H7 / H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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Davis E.O., Henderson P.J.F.;
"The cloning and DNA sequence of the gene xylE for xylose-proton symport in Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
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MEDLINE=87115869; PubMed=3543693;
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01-MAR-1989 (Rel. 10, Last
20-AUG-2001 (Rel. 40, Last
D-XYLOSE-PROTON SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mammalian and bacterial sugar transport proteins are homologous.";
Nature 325:641-643(1987).
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EcoGene; EG11076; xylE.
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"3' end of the maleg operon in E.coli: localization of the transcription termination site.";

Nucleic Acids Res. 16:4097-4109(1988).

-!- FUNCTION: UPTAKE OF D-XYLOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

-!- INDUCTION: BY XYLOSE.
                                                                                                                                                                                                                                                                                                        TRANSMEM
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InterPro; IPR003662; sub_trnsportr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce,
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SEQUENCE OF 1-192
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                       VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAA-SWFG---AVVTLGAA 58
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S00874;
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A27418; A27418.
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S; PR00171; SUGRTRNSPORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUGAR_TRANSPORT_1;
SUGAR_TRANSPORT_2;
                                                                                                                                                                                                   32
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                                                                                            23.0%;
                                                                                                                                                                             53608 MW;
                                                                        87;
                                                                                          Score
Pred.
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A -> V (IN REF. 6).
: 2AF1AF9756C0B722 CRC64;
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                                                                      Mismatches 180;
                                                                                          535.5; DB
No. 8.9e-29
                                                                                                             DB 1;
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AGGVLGGWLVDRAGRKLSLLLCSVPFV-----

IFSITLVATLGGLLFGYDTAVISGTVESLNTVFVAPQNLSESAANSLLGFCVASALIGCI 69

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IGGALGGYCSNREGRRDSLKIAAVLFFISGVGSAWPELGETSINPDNTVPVYLAGYVPEF 129

----AGFAVITAAQDVWMLLGG----- 103

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTR2_RAT STANDARD; PRT; 522 AA. P12336; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) GLUCCOSE TRANSPORTER TYPE 2, LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAT
                             the Buropean Bioinformatics Institute. The use by non-profit institutions as love modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                               This SWI
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                   transporter present
islet cells.";
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89003066; PubMed=3048704;
Thorens B., Sarkar H.K., Kaback H.R., Lodish H.F.;
"Cloning and functional expression in bacteria of a novel glucose
transporter present in liver, intestine, kidney, and beta-pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>1</u>
                                                                                                                                                            MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASM MEMBRANE OF HEPATOCYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE THE BETA CELLS: IT MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. IT MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE & KIDNEY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: PRESENT IN LIVER, INTESTINE, KIDNEY AND BETA-PANCREATIC ISLET CELLS.

SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                  FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY
                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPNATRGKALATAVAAQWLANYFVSWTFPMMDKNSWLVAHFHNGFSYWTYGCMGVLAALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEE--AKFKDSSLASVVVGV1QVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AGWVLE--WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTOHRRQEAIA-LRFLWGSEQG
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 J03145;
 AAA41298.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IVALLSMLFYVAAFAMSWGPVCWVLLSEI
                                              moved. Usage by (See http://www.
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Interpro; IPR003663; Sugar_trnsportr.
Interpro; IPR003662; sub_trnsportr.
Interpro; IPR003662; sub_trnsportr.
Pfam; PF00083; Sugar_tr; 1.
PRINTS: PR00171; SUGRTRNSPORT.
PRINTS: PR00171; SUGRTRNSPORT.
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PRINTS; PRO0172;
PRINTS; PR01191;
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VFFLFAGVVLVFT-LFTFFKVPETKGKSFDEIAAEF
               GAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF
                                                                                                                                            QFSGINGIFYYSTSIFQTAGISQPYYAT1GVGAINMIFTAVSVLLVEKAGRRTLF-LAGM
                                                                                                                                                                  QLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGV
                                                                                                                                                                                                                                          LVTGILISQIAGLSFILGNQDYWHILLGLSAVPALLQCLLLLFCPESPRYLYLNLEEEVR
                                                                                                                                                                                                                                                                  VVVGILLAYLAG--WVL----EWRWLAVLGCVPPSLMLLLMCFMPETPRFL---LTQHRR 192
                                                                                                                                                                                                                                                                                            LTGALLMGCSKFGPAHALIIAGRSVSGLYCGLISGLVPMY1GEIAPTTLRGALGTLHQLA 193
                                                                                                                                                                                                                                                                                                                                                                                            FTAVLGSFQFGYDIGVINAPQEVIISHYRHVLGVP-LDDRRATINYDINGTDTPLIVTPA
                                                                                                                                                                                                                                                                                                                                                                                                                   FAAALGPLSFGFALG-YSSP--AIPSLQRAAPPAPRLDDAAA---------
                                              FLFVSFFEIGPGPIPWFMVAEFFSQGPRPTALALAAFSNWVCNFIIALCFQYIADFLGPY
                                                                                               IGMFFCAVE
                                                                                                                   VMVFSTSAFGAYFKLTQGGPGNSSHVATSAPVSAQPVDASVGL-----AWLAVGSMC--
                                                                                                                                                                                           AKK-SLKRLRGTEDITKDINEMRKEKEEASTEQKVSVIQLFTDPNYRQPIVVALMLHLAQ
                                                                                                                                                                                                                   QEATALRFLWGSEQGWED-----PPIGAEQSFH-LALLRQPGIYKPFIIGVSLMAFQ
                                                                                                                                                                                                                                                                                                                   VAGFAVITAAQ----DVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLM 141
                                                                                                                                                                                                                                                                                                                                                                   -----SW------FGAVVTL------GAAAGGVL----GGWLVDRAGRKLSLLLCSVPF 84
                                                                                                                                                                                                                                                                                                                                            HTTPDAWEEETEGSAHIVTMLWSLSVSSFAVGGMVASFFGGWLGDKLGRIKAMLAANSLS 133
                                                                     -LFTAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPY 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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29.7%;
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Pred. No. 1e-28;
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-LINKED (GLCNAC. . .) (1075AB81E56CF33F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                               -MSLGLVLLDKFTWMSYVSMTAI
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19;

RESULT 14 GTR2_MOUSE

GTR2_MOUSE

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EMBL; X16986; CAA34855.1; -
EMBL; X15684; CAA33719.1; -
EMBL; X7926; AAB20847.1; -
PIR; S06920; S06920
PIR; S05319; S05319.
InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; Sub_trnsportr.
Pfam; Pf00083; Sugar_tr: 1
PRINTS; PR00171; SUGRTRNSPORT.
                                                                  MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucose transporters are differentially expressed in early postimplantation mouse embryos. ;
Development 116:555-561(1992).
                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                          entities
                                                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOGAN A. Heyner S., Charron M.J., Cop. Hogan A., Heyner S., Charron M.J., Cop. Jenkins N.A., Thorens B., Schultz G.A. "Glucose transporter gene expression in Development 113:363-372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90098776; PubMed-2602116;
Suzue K., Lodish H.F., Thorens B.;
"Sequence of the mouse liver glucose transporter.";
Nucleic Acids Res. 17:10099-10099(1989).
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01-FEB-1996
01-NOV-1997
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STRAIN=C57BL/6; TISSUE=Liver;
MEDLINE=89366666; PubMed=2771649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asano T., Shibasaki Y., Lin J.L., Akanuma Y., Takaku F., Oka Y. "The nucleotide sequence of cDNA for a mouse liver-type glucose transporter protein.";
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STRAIN=BALB/C; TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93170163; PubMed=1289053,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                       MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HERATOCYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY MEMBRANE OF HERATOCYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; IT MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. IT MAY ALSO PARTICIPATE WITH THE NATH JUDGOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE & KIDNEY SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN ENDODERM LAYER OF YOLK SAC AND ITURE REPLANSED IN EMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                         SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS, SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                               MGI:1095438; Slc2a2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                        requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acids Res. 17:6386-6386(1989).
                                                                                                                                                                                                                                                                                                                             SPECIFICITY: IN EMBRYO, EXPRESSED AC AND LIVER PRIMORDIUM.
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PRINTS; PR01191; GLUCTRSPORT2.
PROSITE; PS00216; SUGAR_TRANSPORT_2;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
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                     PYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF
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                                                                                                        GVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGL----
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N -> T (IN REF. 2).

S -> T (IN REF. 2).

L -> F (IN REF. 2).

P -> S (IN REF. 1).
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InterPro: IPR003662; sub_trnsportr.
Pfam: PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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Chlorella kessleri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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NCBI_TaxID=3074;
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GWRLSLGLAAVPGLILLLGAIVLPESPNFLVEKGRTDQGRRILEKLRGTSHVEAEFADIV
                                                         EWRWLAVLGCVPPSLMLLLMCFMPETPRFLL----TQHRRQEATALRFLWGSEQGWED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLAAFAAALGPLSFGFALGYS---SPAIPSLQR----
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                                                                                                                                                                                                     GSASSAALLNTVVVGAVNVGSTMIAVLLSDKFGRRFLLIEGGITCCLAMLAAGITLGVEF
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Search completed: February 13, 2002, 22:06:05 Job time: 861 sec

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Post-processing: Minimum Match 0%
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Copyright (c) 1993
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Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

19	18	17	16	15	14	13	12	11	10	9	· œ	7	ø	ر ح	4	ω	2	1	No.	Result
637.5	656	692	708.5	717.5	717.5	725.5	730	753	777	780.5	927	2040.5	2041.5	2047.5	2050.5	2057	2298.5	2301.5	Score	
27.4	28.2	29.8	30.5	30.9	30.9	31.2	31.4	32.4	33.4	33.6	39.9	87.8	87.8	88.1	88.2	88.5	98.9	99.0	Match Length	Olberv
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Q9vnj2 drosophila	Q9v3g0 drosophila	Q9vnj1 drosophila	Q9xhw3 oryza sativ	Q39416 beta vulgar	Q9v848 drosophila	Q9frl3 arabidopsis	Q9ln48 arabidopsis	Q9v610 drosophila	Q9v609 drosophila	Q9vu17 drosophila	Q9ugq3 homo sapien		mus	Q9jif3 mus musculu	Q9jjp4 mus musculu	Q9jjz1 rattus norv	Q9nsc4 homo sapien	Q9ny64 homo sapien	Description	

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61 GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120

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45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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081492	Q9LKH2	Q9FRT5	081501	Q06312	Q40373	Q9M100	Q9FXY8	Q9FRP7	Q9DBA7	Q9LLE2	005182	Q9LF13	Q9LLD9	Q9LLE0	Q9F1F2	Q9SCW9	P96710	Q9LLD8	Q9LLE1	P96742	065322	Q9C757	065799	022848	Q9MAA4
O81492 arabidopsis	Q91kh2 mesembryant	Q9frt5 oryza sativ	O81501 arabidopsis	Q06312 nicotiana t	Q40373 medicago tr	Q9m100 arabidopsis	Q9fxy8 mesembryant	Q9frp7 oryza sativ	Q9dba7 mus musculu	Q9lle2 spinacia ol	005182 bacillus me	Q91f13 arabidopsis	Q911d9 zea mays (m	Q911e0 solanum tub	Q9fif2 arabidopsis	Q9scw9 arabidopsis	P96710 bacillus su	Q911d8 arabidopsis	Q9llel nicotiana t	P96742 bacillus su	065322 petunia hyb	Q9c757 arabidopsis	065799 arabidopsis	022848 arabidopsis	Q9maa4 arabidopsis

## ALIGNMENTS

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Db
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                                                                                                                                       Query Match 99.0
Best Local Similarity 99.1
Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Toberson M.R., Uldry M.A., Thorens B.;

"GLUTXI: A novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";

J. Biol. Chem. 275:4607-4612(2000).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE LOCATION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION (BY SIMILARITY).
-!- SUBCELL
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O9NY64: O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN_2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                            Transmembrane.
SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUTX1.
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MEDLINE=20138191; PubMed=10671487;
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                                 RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG 60
RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG 83
                                                                                                                                                                                                                                                                                                                            AA;
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99.1%;
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Pred. No. 1.1e-122;
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Best Local Similarity
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Doege H., Schuermann A., Bahrenberg C., Brauers A., Joo Doege H., Schuermann A., Bahrenberg C., Brauers A., Joo Googe H., Schuermann A., Bahrenberg C., Brauers A., Joo Joo Does H., Schuermann A., Bahrenberg C., Brauers A., Joo Joo Does H., Schuermann A., Bahrenberg C., Brauers A., Joo Joo Joo Does H., Joo 
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Q9NSC4;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
GLUCOSE TRANSPORTER 8.
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pRINTS: pR00171; SUGRTYRNSPORT_1:
pROSITE: pS00216: SUGAR_TRANSPORT_1:
pROSITE: pS00217: SUGAR_TRANSPORT_2:
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Mammalia; Eutheria; Primates;
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Pred. No. 1.7e-122;
1; Mismatches 2;
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Last annotation update)
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Q9JJZ1;
01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                             Tbberson M.R., Uldry M.A., Thorens B.;

"GLUTXI: A novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues.";

J. Biol. Chem. 275:4607-4612(2000).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL; AUX4935; CAB75729.1;

InterPro; IPR003662; sub_transporter.

InterPro; IPR003663; Sugar_transporter.
                                                                                                                                                                               pfam: pF00083; sugar_tr: 1.
pRINTS: pR00171; SUGRTRNSPORT.
pROSITE: pS00216; SUGAR_TRANSPORT_1;
pROSITE: pS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                            Transmembrane. SEQUENCE 478
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCOSE TRANSPORTER
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                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia;
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Pred. No. 7.1e
32; Mismatches
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Q9JJP4;
Q9JJP4;
01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
GLUCOSE TRANSPORTER 8.
GLUTX1 OR GLUT8.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD: MGI:1860103; GlutX1.
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane.
SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM: PF00083; sugar_tr; 1
PRINTS: PR00171; SUGATRNSPORT.
PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2.
PROSITE: PS00217: SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucose transport activity.";
J. Biol. Chem. 275:16275-16280(2000).
-i- SUBCELULIAR LOCATION. INTEGRAL MEMBRANE PROTEIN
-i- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20283667; PubMed=10821868;
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                       YISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMP
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Pred. No. 1.6e-108;
Pred. No. 29;
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                                                                                                                                                                                                                             pfam; pF00083; sugar_tr; 1.
pRINTS; pR00171; SUGRTRNSPORT.
pROSITE; pS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
pROSITE; pS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20319023; PubMed=10860996; Carayannopoulos M.O., Chi M.M.Y., Cui Y., Pingsterhaus McKnight R.A., Mueckler M., Devaskar S.U., Moley K.H.; "GLUT8 is a glucose transporter responsible for insulin
                                                                                                                                                                                                            Transmembrane. SEQUENCE 477
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YISEIAYPAVRGLLGSCVQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMP
                                                              GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120
                                                                                                            RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG 60
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                                                                                                 RRVFLASFAAALGPLSFGFALGYSSPAlpSLRRTAPPALRLGDNAASWFGAVVTLGAAAG
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86.4%;
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Pred. No. 2.4
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Best Local
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Q9JJZ0;
Q1-OCT-2000
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InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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01-JUN-2001 (TrEMBLrel.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCOSE TRANSPORTER.
                                                                                                                                                                                               Transmembrane.
SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                Ibberson M.R., Uldry M.A., Thorens B.;
"GLUTX1: A novel mammalian glucose transporter expressed
central nervous system and insulin-sensitive tissues.";
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20138191; PubMed=10671487; Ibberson M.R., Uldry M.A., Thorens
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                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                   PROSITE; PS00216; PROSITE; PS00217;
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                                                                                                  ALSGVIMVFSMSAFGTYFKLTQSLPSNSSHVGL-VPIAAEPVDVQVGLAWLAVGSMCLFI
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                              YISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMP 180
ETPRFLLTQHRRQEAI-ALRFLWGSEQGWEDPPIGAE-QSFHLALLRQPGIYKPFIIGVS
                   YISEIAYPAVRGLLGSCVQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMP
                                                                                                                                             Similarity 85.991; Conservative
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SUGAR_TRANSPORT_2;
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85.9%;
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Last annotation updat
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                                                                                                                                            Score 2041.5; DB 1
Pred. No. 5.3e-108;
2; Mismatches 29;
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                                                                                                                                                                                                14FF23DB9060DAF1 CRC64
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                                                                                                                                                                DB 11; Length 477;
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Best Local
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
GLUCOSE TRANSPORTER 8.
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGATRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                 Transmembrane. SEQUENCE 479
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: INTEGRAL ME-!- SIMILARITY: TO SUGAR TRANSPORTER EMBL; AB033418; BAA94383.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                        GGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAP
                                                                                                                                                                                                                       RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAA-
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                                                    PETPRFLLTQHRRQEAI-ALRFLWGSEQGWEDPPIGAE-QSFHLALLRQPGIYKPFIIGV
                                                                                         VYISEIAYPAVRGLLGSCVQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYM
                                                                                                      VYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFM
                                                                                                                                           GAVLGGWLLDRAGRKLSLLLCTVPFVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAP
                                                                                                                                                                                                RRVFLATFAAALGPLSFGFALGYSSPAIPSLRRTAPPALRLGDTAASWFGAVVTLGAAAQ
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                                      PETPRFLLTQHQYQEAMAALRFLWGSEEGWEEPPVGAEHQGFQLAMLRRPGVHKPLIIGI
                                                                                                                                                                                                                                                  389;
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                  Conservative
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a; Chordata;
                                                                                                                                                                                                                                                                                                                   51601 MW;
                                                                                                                                                                                                                                                  87.8%; Score 2040.5; DB
85.3%; Pred. No. 6e-108;
tive 32; Mismatches 3
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                   EAB2B67B8CDD2FCF CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doege H., Bocianski A., Joost H.G., Schuermann A.;

"Activity and genomic organization of human glucose transporter (GLUT9), a novel member of the family of sugar-transport facility predominantly expressed in brain and leucocytes.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL. AJ011372; CAB66155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UGQ3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00216: SUGAR_TRANSPORT_1: PROSITE: PS00217: SUGAR_TRANSPORT_2: Sugar_transport: Transmembrane. SEQUENCE 507 AA: 54569 MW: 1FC6E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of a sugar transporter gene, a G-beta three novel genes in human chromosome 9q34."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DBJ of the EMBL/GenBank/DDBJ of the E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
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InterPro; IPR003663; Sugar_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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                                                   YISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMP
                                                                                                                                   GVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPV 120
                                                                                                                                                                                                                                                                       RRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAG
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YVSETAPPGVRGALGATPQLMAVFGSLSLYALGLLLPWRWLAVAGEAPVLIMILLLSFMP
                                                                                                            GLSAMILNDLLGRKLSIMFSAVPSAAGYALMAGAHGLWMLLLGRTLTGFAGGLTAACIPV
                                                                                                                                                                                                                    KRVFLATEAAVLGNFSFGYALVYTSPVIPALERSLDPDLHLTKSQASWFGSVFTLGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y17803; CAB96996.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                 Conservative
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RA Beeson K.Y. Benos P.V. Bernan B.P. Bhandari D. Bolshakov S.,

Borkova D. Botchan M.R. Bouck J. Brokstein P. Brottier P.,

RA Burtis K.C. Busam D.A. Butler H., Cadieu E., Center A., Chandra I.,

RA Gherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Dew I., Dietz S.M.,

RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA FOSler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Weilliams S.M., Woodaye T., Weirley K.C., Wu D., Yang S., Yao Q.A.,

Ph., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,

Zheng L.,
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Q1-MAY-2000
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Beeson K.Y.,
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Eukaryota; Metazoa; Arthropoda; Tracheata;
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Benos P.V., Berman B.P., Bhandari D., Bo
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B A., Galle R.F.,
Barson S.N.,
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Baldwin D.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
'International Control of the Profice of Profice 287:2185-2195(2000). INTEGRAL MEMBRANE PROTEIN
'- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL: AE003540; ABF49874.1; -
 MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A.,
                           STRAIN-BERKELEY;
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
SEOUENCE 539 AA; 58413 MW; A2F4814DBF676BBD CRC64;
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                                                               NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                   485 GLGIGGTFWLFAGLTVVGVIFVYFAVPETKGKSLNEIQQELAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 PIGFLINMIGRKWTMLFLVLPFILGWTMLIWAVNVSMLYASRFILGIAGGAFCVTAPMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 FLAAFAAALGPLSFGFALGYSSPAIPSL-QRAAPPAPRLDDAAASWFGAVVTLGAAAGGV
                                                                                                                                                                                                                                                                                VLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEG
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                                                                                                                                                                                                                                                                                                                              AVGSMCLFTAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRFLLTQHRRQEAI-ALRFLWGSEQGWE-----DPPIGAEQSFHLALLRQPGIYKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 122
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                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90; Mismatches 166;
                                                                                                                                                   Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                      489
 Evans
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C.A.,
                                                                                                                                                     update)
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 Gocayne J.D.,
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                                      210
                                                                                                                                                                                                                                                                                                       489 AA; 53026 MW;
                                                                                                                                                                                                                                          Conservative
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RA Allahi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Mopherson D. R. RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M., Ra Palazzolo M., Pittman G.S. Pan S., Pollard J., Puri V., Reese M.G., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Romert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., She B.C., Stolen K., Sunders R.D.C., Venter E., Wang R., Sun E., Syradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Syirskass R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Ye J., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X., Weinser S.M., Wenter J.C., Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Ribbs R.A., Myers E.W., Zhong W., Zhou X., Zhu X., Smith H.O., Ra Zience 287:2185-2195(2000).

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Palybase; FB90033643; CG7801.
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Talali M., Valueb E. K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Talali M., Valueb E. K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Talali M., Valueb E. K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Talali M., Valueb E. K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Berman B.P., Bhandari D., Bolshakov S., Berthan B.P., Barthard B.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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prints; pr00171; SUGRTRNSPORT.
pr0SITE; pS00216; SUGAR_TRANSPORT_1;
pr0SITE; PS00217; SUGAR_TRANSPORT_2;
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InterPro; IPR003663; Sugar_transporter.
233 FIIGVSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLASVVVGVIQVLFTAVAALIMDR
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37.2%; pred. No. 1.1e-36;
76: Mismatches 182;
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Musny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.";
CC -i- SUBCELLULAR 100ATION.
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A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Markullo G., Milshina N., McCharry C., McCleod M.P., McChenofi.
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01-MAY-2000 (TrE
01-JUN-2001 (TrE
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   Science
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   SUBCELLULAR LOCATION:
SIMILARITY: TO SUGAR
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TRANSPORTER
INTEGRAL MEMBRANE PROTEIN
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Best Local :
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Q9LN48;
Q1-OCT-2000
01-OCT-2000
01-JUN-2001
                          Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
"Genomic I.";
                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptha; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                  F18014.22.
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SEQUENCE 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0033644; CG8234. InterPro; IPR003662; Sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003825; AAF58630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNWFCTFVVTKTFQDLTVAMGAHGAFWLFGAICIVGLFFVIIFVPETRGKSLEETERKMM
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             sequence
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             for Arabidopsis thaliana
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38.2%;
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               BAC F18014 from chromosome
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                                                                                                Lee J.,
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Best Local Similarity
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL; AC025808: AAF79445.1;
-InterPro: IPR003662: snh +--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003663; Sugar_transporter pfam; pF00083; sugar_tr; 1. pfam; pF00083; Sugar_tr; 1. Sugar_trsport; pR10171; Sugar_trsport; pr00216; Sugar_transport_1; uprosite; ps00217; Sugar_transport_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
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 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000)
                                                                                                                                                                                                                                                                210
                                                                                                                                                                                                                                                                                                                                                      165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV
                                                     GSIATLLNWFVSWLVTMTANMLL-AWSSGGTFTLYALVCGFTVVFVSLWVPETKGKTLEE
 IQALF 514
                         ITAHF 450
                                                                              TGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQ
                                                                                                                 SNMYNILSMVS---
                                                                                                                             SSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVA
                                                                                                                                                                      SSNVATFGVGVVQVVATGIATWLVDKAGRRLLLMISSIGMTISLVIVAVAFYLKEFVSPD
                                                                                                                                                                                                  DSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGN
                                                                                                                                                                                                                               FDRSVASSSKRSAVRFVDLKRRRYYFPLMVG1GLLALQQLGGINGVLFYSST1FESAGVT
                                                                                                                                                                                                                                                                                        PRWLVCLYNRIAYIVEEVALLAKMGLTDDFETSLQVLRGFETDITVEVNEIKVVTKLKKC
                                                                                                                                                                                                                                                                                                                     PRFLLTQHRR----QEATALRFLWGSEQGWE--------
                                                                                                                                                                                                                                                                                                                                                                   SEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPET
                                                                                                                                                                                                                                                                                                                                                                                                          ASGQIAEYVGRKGSLMIAAIPNIIGWLSISFAKDTSFLYMGRLLEGFGVGIISYTVPVYI
                                                                                                                                                                                                                                                                                                                                                                                                                            VLACVLIVALGPIQFGFTCGYSSPT----QAAITKDLGLTVSEYSVFGSLSNVGAMVGAI
                                                                                                                                                                                                                                                          -DPPIGA----EQSEHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFK
                                                                                                                                                                                                                                                                                                                                                   AEIAPQTMRGALGSVNQLSVTIGIMLAYLLGLEVPWRILAVLGVLPCTLLIPGLFFTPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; 36.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                              --VVGVVAMVIS-CSLGMGPIPWLIMSEILPVNIKGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 730; DB 10; Pred. No. 5.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80574480E64EF8D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                      509
                                                                                 445
                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                   224
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                                                                                                                                                                        404
                                                                                                                                                                                                                               344
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RESULT 13
Q9FRL3
ID Q9FRL3
AC Q9FRL3
AC Q9FRL3
DT 01-MAR
DT 01-MAR
DT 01-MAR
DT 01-MAR
DT 01-MAR
OC Arabid
OC Eukary
OC Sperma
OC SPERMA
OC STRAIN
RA MAİTİ
RA MAİTİ
RA BARNSİ
RL SUBMİT
CC -!- SI
DR EMBL;
DR INTERF
DR INTERF
DR Pfam;
DR Pfam;
DR PFANSI
SQ SEQUEN
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ALLIN X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

AMAITI R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,

Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;

Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence.";

L. Submitted (JAM-2001) to the EMBL/GenBank/DDBJ databases.

C. -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

BEMBL; AC025814: AAG12689.1; --

BR InterPro; IPR00366; Sub_transporter.

RITHERPOSITE: PR001363; Sugar_tr: 1.

RR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FRL3 PRELIMINARY; PRT; 487 AA.

Q9FRL3;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTEGRAL MEMBRANE PROTEIN, PUTATIVE, 33518-36712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
SEQUENCE 487
 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV
AWSSGGTFTLYGLVCAFTVVFVTLWVPETKGKTLEELQSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI
                                                                                                                                                                                                               YFPLMVGIGLLVLQQLGGINGVLFYSSTIFESAGVTSSNAATFGVGAIQVVATAISTWLV
                                                                                                                                                                                                                                                                                                                                                                              VLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF
                                                                     SVVGVVAMVVFFSLGMGPIPWLIMSEILPVNIKGLAGSIATLANWFFSWLITMT-ANLLL
                                                                                       AVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLME
:| : |::| | | | | | | | ::|:| ::|:
                                                                                                                                            DKAGRRLLLTISSVGMTISLVIVAAAFYLKE
                                                                                                                                                                              DRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWL
                                                                                                                                                                                                                                                                                      PRWLAKMGMTDEFETSLQVLRGFE---TDITVEVNEIKRSVASSTKRNTVRFVDLKRRRY
                                                                                                                                                                                                                                                                                                                                                             AEIAPQNMRGGLGSVNQLSVTIGIMLAYLLGLFVPWRILAVLGILPCTLLIPGLFFIPES
                                                                                                                                                                                                                                                                                                                                                                                                                                     ASGQ1AEYIGRKGSLMIAAIPNIIGWLCISFAKDTSFLYMGRLLEGFGVGIISYTVPVYI
                                                                                                                                                                                                                                                   YKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIM
                                                                                                                                                                                                                                                                                                                          PRFLLTQHRRQE-AIALRFLWGSEQGWEDPPIGAEQ-----SFHLALLRQPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLACVLIVALGPIQFGFTCGYSSPT----QAAITKDLGLTVSEYSVFGSLSNVGAMVGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 AA; 52901 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%;
ilarity 37.5%;
Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 725.5; DB 1
Pred. No. 9.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98604E3642914472 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176;
                                                                                                                                            --FVSPDS
486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                          229
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RA Abril J.F. Agbayani A., An H.-J. Madrews-Pfankoch C. Baddwin D.,
RA Abril J.F. Agbayani A., An H.-J. Madrews-Pfankoch C. Baddwin D.,
RA Belson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtls K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syier E., Spradling A.C., Stapleton M., Skupskin M.P., Smith T.,
RA Syier E., Spradling A.C., Stapleton M., Skupskin M.P., Smith T.,
RA Syier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sines S.M., Wooldage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.M., Wayers E.W., Rubin G.M., Venter J.C.,
The Gene 287:2185-2195(2000)
ô
                                                  Query Match
Best Local Sin
Matches 159;
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Q9V848;
01-MAY-2000
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Préifier B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG6484
CG6484
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Pterygota; Neoptera; Endopterygota; Di
Ephydroidea; Drosophilidae; Drosophila
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01-JUN-2001
                                                                                                                                                                                                                                                                            Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
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                                                                                                                                                                                                       fransmembrane
                                                                                                                                                                                                                               PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                       PROSITE; PS00216; SUGAR_TRANSPORT_1;
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003662; sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003802; AAF57829.1; -
FlyBase; FBqn0034247; CG6484.
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                            InterPro; IPR003663; Sugar_transporter.
4 FLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
                                                                          Similarity
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                  AΑ;
                                                                                                                                                                               50271 MW;
                                                                          30.9%;
34.9%;
                                                  95;
                                                                          Score 717.5; DB 5
Pred. No. 2.5e-33;
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                                                                                                                                                                               004B4CACF406BDBB CRC64;
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                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465
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                                                                                                     DB 5;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insecta;
                                                  29;
                                                  Gaps
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Best Local Similarity
                                                                                                                                                                                                                               Matches
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01-NOV-1996
01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta vulgaris (Sugar beet)
Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caryophyllidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
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                                                                                                                                                                                                                               167;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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pfam; pF00083; sugar_tr; 1,
pROSITE; pS00216; SUGAR_TRANSPORT_1;
pROSITE; pS00217; SUGAR_TRANSPORT_2;
Sugar transport; Transmembrane.
sequence 490 AA; 53020 MW; 3F8C96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendel; 16093; Betvu;2447;16093.
InterPro; IPR003662; sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY. EMBL; U43629; AAB53155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 GPGPTFWIFTAIAVIAFFYSLFFVPETKGKTIIEI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 RPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI 446
106 ASGQISEYIGRKGSLMIAAIPNIIGWLAISFAKDSSFLYMGRMLEGFGVGIISYTVPVYI
                                                         63 LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 122
                                                                                                                                                                                          VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDS-SLASVVVGVIQVLFTAVAALIMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSICIFIIFFSIGFGPVPWLVMAELFSEDVKSVAGSIAGTSNWLSAFVVTLLFPILKSSI 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYLAMKGRNDDAAKALQWLRGKDADIDDELKEILEESQKQIDMPQVNILSSLRRPIVLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGIAVLLQVFQQWTGINAVLFYSASIFEDTGSDISGSDATLIIGVTQVTSTLVAVAIIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFLLTQHRRQEAI-ALRFLWGSEQGWED-----PPIGAEQSFHLALLRQPGIYKP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGWLYDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YIAGLSASFGALCMGASIGWSSPVENMITVNTEYGFPISSSQFGWVSSLLTLGATVICIP
                                                                                                                             VLACVLIVALGPIQFGFTAGYSSPT----QSAITNELGLSVAEYSWFGSLSNVGAMVGAI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGRRILLLISGYLMAVSTALMGVYFQLKENDPASMDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EITATALRGTIGSFFQLLIVSGVLYGYLVGAFLPLLTINILCAILPVIFAIIHFFMPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGFAIDWIGRRPTMLALIPPYMVGWVLMLFAKNVTMLYFGRFILGMCGGAFCVTAPMYCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caryophyllales; Chenopodiaceae; Beta
                                                                                                                                                                                                                                                                                         30.9%;
36.1%;
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                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                           Score 717.5;
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                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                            No. 2
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                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                       Length 490;
                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                          Gaps
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Search completed: February 13, 2002, 22:04:42 Job time:  $863\ \text{sec}$ 

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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein .
                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     627
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_1101:*
1: /SIDS2/gcgdata,
2: /SIDS2/gcgdata,
3: /SIDS2/gcgdata,
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                                                                                                                                                                                                                                                                                                                                                                          1: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: IDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp/AA1992.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp/AA1996.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WRPLZNZWIPRAAGIRHELV.....VTGSPELSWLRVSKGVEWPQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     February 13, 2002, 21:50:11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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                      AAB66941
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AAB45158
AAY95032
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                                                                                                              AAE04888
AAB66932
                                                                                                                                                 AAB66939
AAB66934
                                                                                                                                                                                     AAB66933
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GLUTX3 consensus s
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Rat GLUTX3. Rattu
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GLUTX1 consensus s
Murine GLUTX1. Mu
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Human GLUTX3. Hom
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	AAG16799	AAG16800	AAG52315	AAG52316	AAG52317	AAG06141	AAG06142	AAG06143	AAG39281	AAG39282	AAG39283	AAG10665	AAG10666	AAG10667	AAG30432	AAG30433	AAG30434	AAG48644	AAG48645	AAG48646	AAY02168	AAG38869	AAG20976	AAG13748	AAG38870	AAG20977	AAG13749	AAG38871	AAG20978	AAG13750	AAG37420	AAG37398	AAG37422	AAG37400
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## ALIGNMENTS

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AAB66933
                                                                      14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                                                                          Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
        N-PSDB; AAF55866
                                                                                                                                                                                                                                                   17-APR-2001
                  WPI; 2001-112615/12
                                   Thorens B, Ibberson M,
                                                                                                                   14-JUL-2000; 2000WO-IB01042.
                                                                                                                                      18-JAN-2001
                                                                                                                                                        WO200104145-A2
                                                                                                                                                                                                                                 Rat GLUTX1.
                                                                                                                                                                                                                                                                    ААВ66933;
                                                                                                                                                                                                                                                                                       AAB66933 standard; Protein;
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                                                     UNIV LAUSANNE
                                                                      99US-0143907.
99US-0151140.
2000US-0184285.
2000US-0616132.
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                                   Uldry M;
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AAB66938

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Best Local S
Matches 118
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27-AUG-1999;
23-FEB-2000;
The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative
                                                                                                                           Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                        Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; murinc hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
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99US-0151140.
2000US-0184285.
2000US-0616132.
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                                                                                124pp; English.
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. 3.1e-64;
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Best Local :
                                                                                                                           Nucleic acids encoding GLUTX glucose transporter proteins, the prevention, diagnosis and treatment of hexose transport e.g. ischemia and diabetes -
                                                                                                                                                                        WPI; 200
N-PSDB;
                                                                                                      Claim 11; Page 73-74; 124pp; English.
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23-FEB-2000;
                                                                                                                                                                                                                                                                                                   14-JUL-2000; 2000WO-IB01042
                                                                                                                                                                                                                                                                              14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                             WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                    hypoglycaemia; glucose metabolism disorder; neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                           Murine; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                Murine GLUTX1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence.
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DB; AAF55867.
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2000US-0184285.
2000US-0616132.
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93.2%;
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.2e-61;
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The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is murine GLUTX1.

Sequence

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RESULT
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Best Local S
Matches 107
                                                                                                 28-JAN-2000;
02-FEB-2000;
10-FEB-2000;
                                                                                                                                 23-DEC-1999;
14-JAN-2000;
21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
WPI; 2001-418042/44
N-PSDB; AAD09552.
                                                                                                                                                                                                                                                                                Domain
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                              Hillman JL, Az
Tang YT, Khan
                                                                                                                                                                                                     28-JUN-2001
                                                                                                                                                                                                                          WO200146258-A2.
                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia, depression; Alzheimer's disease; epilepsy; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
                                                                                                                                                                               22-DEC-2000; 2000WO-US35095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
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                                                      MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis;
                                                                            INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                      Burford
                                                                                                           2000US-0176083.
2000US-0177332.
2000US-0178572.
2000US-0179758.
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                                          Azimzai
                                                                                                 2000US-0181625
                                                                                                                                                                                                                                                                                                                                                                                                        syndrome; hypercholesterolaemia; cancer.
                                                                            GENOMICS.
                                                                                                                                                        99US-0172000
                                                                                                                                                                                                                                                          /label=
438..457
                                                                                                                                                                                                                                                                               /label= T
320..339
                                                                                                                                                                                                                                                                                                    /label=
293..313
                                                                                                                                                                                                                                                                                                                            /note=
259..2
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 29..474
                                                                                                                                                                                                                                                 /label=
                                    , Y, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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90.7%;
                                                                                                                                                                                                                                                                                                                             .279
                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                      "Sugar transporter domain"
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                                                                                                                                                                                                                                                                   Transmembrane_domain
                                                                                                                                                                                                                                                                                          Transmembrane_domain
                                                                                                                                                                                                                                                                                                                Transmembrane_domain
                                                   Au-Young J,
                                           Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477
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Pred.
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                                          Nguyen
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No. 6.1e-60;
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                                                    DAM,
                                           DB,
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                                           Yao
                                          Yang J
Yao MC,
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                                                    J,
                                           Gandhi
                                                      Reddy
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Length 477;

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glucose-galactose malabsorption syndrome, hyperopsoriasis and viral, bacterial, fungal, helmintlinfections. TRICH DNA is useful in gene therapy
                                                                                                                                    sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                                         including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatomyositis, arrhythmias and asthma and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle disorder including cardiomyopathy, myocarditis, polymyositis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 112-113; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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Sequence
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder including amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is transporter and ion channel-1 (TRICH-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins useful for treating muscle and immunological
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AAB66932
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Best Local
14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                              14-JUL-2000;
                                                                                                                                                                                                                     Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                              AAB66932;
                                                                                                            18-JAN-2001
                                                                                                                                      WO200104145-A2
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                    hypoglycaemia;
                                                                                                                                                                                                                                                                  Human GLUTX1
                                                                                                                                                                                                                                                                                                 17-APR-2001
                                                                                                                                                                                                                                                                                                                                                             AAB66932 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      81 WFMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAH 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PISAEPADVHLGLAWLAVGSMCLEIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 84.9
98; Conservative
99US-0143907.
99US-0151140.
2000US-0184285.
2000US-0616132.
                                                                              2000WO-IB01042
                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                    glucose metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.8%;
84.5%;
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders.
                                                                                                                                                                                                                                                                                                                       Human GLUTX3
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                                                                                                                                                                                                                                                                                                                                                                                         AAB66937 standard;
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                                                                                             (UYLA-) UNIV LAUSANNE
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                                                                                                                                                                                                    18-JAN-2001
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                                                                                                                                                                                                                                                                        hypoglycaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                 sapiens
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                                               2001-112615/12.
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                                                                                                                                                                                                                                                                    GLUTX; gene therapy; vaccine; hexose transport modulator; transport disorder; ischaemia; diabetes; hyperglycaemia; ycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                      В,
                                     AAF55870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                  99US-0143907.
99US-0151140.
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2000US-0616132.
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                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \ensuremath{\text{\textbf{n}}}, diagnosis and treatment of hexose transport disorders and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑĄ;
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82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                        e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
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                                                                  Claim
                                                                                                                                            Nucleic acids encoding GLUTX glucose transporter prevention, diagnosis and treatment of hexose e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUTX3 consensus sequence
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                                                                  11; Page
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; 2000US-0184285.
; 2000US-0616132.
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                                                                  83-84;
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No. 4.7e-24;
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e transport
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                                                                                                                                                                                       disorders,
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The present invention relates to GLUTX proteins (AAF55865-AAF55871 and

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RESULT
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Best Local S
Matches 59
                                                                                                                                                                         25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
23-AUG-1999;
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                          Claim 87;
                                                                                                                                                                                                                                   24-AUG-1998;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                              02-MAR-2000
                                                                                                                                                                                                                                                                                                                                     WO200011015-A1
                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein vql_1, SEQ ID NO:78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2000
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                                                                                                                        Valenzuela D,
                                                                                                                                               (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                         28-SEP-1998;
                                                                                                                                                                                                                                                             24-AUG-1998;
                                                                                                                                                                                                                                                                                     24-AUG-1999;
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                                                            secreted or transmembrane proteins and polynucleotides encoding m, useful for treating neurodegenerative disorders, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGIRHELVPISAEPADVHLG-LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFFLHIKGV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 45.7 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                      98US-0102092.
98US-0109978.
98US-0113645.
98US-0113646.
98US-0379246.
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                                                                                                                        Yuan O,
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                          335-336;
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98US-0099618
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  to
                       357pp; English.
                                                                                                                         Hoffman
40 human secreted proteins
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                                                                                                                       Rapiejko
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                                                                                                                                                                                                                                                                                                              Human; secreted protein; immunosuppressive; antiarthritic; antirheumaticantiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activin/inhibin activity; chemotactic/chemokinetic activity; haem and thrombolytic activity; anti-inflammatory activity; and tumour
               Rosen CA,
                                                                                       26-MAR-1999;
17-DEC-1999;
                                                                                                                                                                                   05-OCT-2000
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                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                nervous
                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein sequence encoded by gene 39 SEQ ID NO:99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB45158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB45158 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulation; haematopoiesis regulation; tissue growth activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine activity; cell proliferation; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and cDNA sequences encoding them (AAA23423-A23462). The secreted
                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                              22-MAR-2000; 2000WO-US07505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin dependent diabetes mellitus; and allergic reactions such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 pffffaaiclvslvftgccvpetkgrslegiesffrtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system
                 Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AA;
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                                                                                                                                                                                                                                                                                              disorder;
disorder;
                                                                                       99US-0126502.
99US-0172410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.3%;
53.1%;
                 Komatsoulis G;
                                                                                                                                                                                                                                                                                              aging;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 278; DB 21;
Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic;
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RESULT 1
AAY95032
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AC AAY9
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DE Huma
XX Huma
KW Infe
KW ORF;
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XX ONE
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24-AUG-1999;
                                                                 02-MAR-2000
                                                                                                                           WO200011015-A1
                                                                                                                                                                                                                                                                                                           Human: secreted protein; cancer; tumour; cardiovascular disorblood disorder; haemophilia; autoimmune disease; diabetes; in infection; fungal; bacterial; viral; HIV; allergy; arthritis;
                                                                                                                                                                                                                                                                                             neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY95032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAB45119 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human clone vql_l insertional variant ORF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY95032 standard; Protein; 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage capabilities. used in the isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. rheumatoid arthritis, hyperprollierative disolvers e.g. cardiac arrest, of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral isochaemia, angiogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 AFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 lfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvltksflpvvstfglqv 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their activities include immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 396; 440pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
99WO-US19351
                                                                                                                                                                                                                                                                                      disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.3%; Score 278; DB 21; 53.1%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                 inflammation;
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insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. Sequences AAY95024-Y95025, AAY95029 and AAY95031-Y95032 represent additional open reading frames (ORFs) that are
                                                                                                                                                                                                                                        regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1998;
24-AUG-1998;
09-SEP-1998;
28-SEP-1998;
28-SEP-1998;
25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                         encoded by deletional or insertional variants of
                                                                                                                                                                                                                                                                                                                                                                   inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                   and thrombolytic activity; anti-inflammatory activity; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 351-352; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG
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  147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0097638.
98US-0097659.
98US-0099618.
98US-0102092.
98US-0103645.
98US-0113646.
98US-0379246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rapiejko
                                                      4-Y95025, AAY95029 and g frames (ORFs) that ar the cDNA clones of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
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Best Local Similarity
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                        AAB66938;
                                                 AAB66938
                                                                                                                                       103 AFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDGPLSVTG-SPEL
                                                                                                                                                                              43 LFIAGFAVGWGDIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 102
                                                                                                            62 pffffaaiclvslvftgccvpetkgrsleqiefllphgekvllalgggprl
                                                                                                                                                             2 lfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvltksflpvvstfglqv 61
                                                standard; Protein; 503 AA
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                   31.0%;
                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                  Score 275.5; DB 21;
Pred. No. 4.1e-24;
Pred. No. 4.1e-24;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                              Length
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17-APR-2001

(first entry)

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RESULT
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Best Local
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention are treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX3.
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   hybridisation assay; genetic mapping; gene expression control;
                   Protein identification; signal transduction pathway; metabolic
                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 45980
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                                                                                                                                            AAG37400 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 82-83; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leic acids encoding GLUTX glucose transporter proteins, useful in prevention, diagnosis and treatment of hexose transport disorders, ischemia and diabetes -
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                  pathway;
 promoter;
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Best Local S
Matches 53
             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana
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13-OCT-1999;
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                                                                                                                                                                                                                                                                     l Similarity
53; Conserv
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                                                          thaliana protein fragment SEQ ID NO: 46010.
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 Matches

40;

Conservative

22;

Mismatches

Indels

1;

Gaps

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Ouery Match  Ouery Match  20.6%; Score 183.5; DB 2; Length  Best Local Similarity 37.7%; Pred. No. 2e-13;  Marches 40: Conservative 22: Mismatches 43: Indels	RESULT 1 US-09-031-392-10 US-09-031-392-10 US-09-031-392-10  Sequence 10, Application US/09031392 Patent No. 5942398 GENERAL INFORMATION: APPLICANT: Waeng, Xun APPLICANT: Waeng, Xun APPLICANT: Waeng, Xun APPLICANT: Waeng, Xun APPLICANT: Waeng, Xun APPLICANT: Waeng, Xun ITILE OF INVENTION: ENCODING GLUTEX AND USES THEREOF NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110-2804 COMPUTER: LAN COMPUTER: LAN COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: LAN COMPUTER: LAN COMPUTER: LAN COMPUTER: LAN COMPUTER: DISKETING OPERATING SYSTEM: Windows Version 2.0 CURRENT APPLICATION NUMBER: US/09/031,392 FILING DATE: 26-Feb-1998 ATTORNEY/AGENT INFORMATION: NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35.283 REFERENCE/DOCKET NUMBER: 07334/072001 TELEFAX: 617/542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 493 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: protein	ALIGNMENTS	28 74 8.3 632 4 US-09-343-361-10 29 74 8.3 632 5 PCT-US93-01959-10 30 73 8.2 520 4 US-08-964-127-2 31 72.5 8.1 817 1 US-08-381-931B-2 32 72 8.1 430 1 US-08-919-624-3 33 72 8.1 430 2 US-08-919-624-3 34 72 8.1 450 1 US-08-029-170-23 35 72 8.1 450 1 US-08-029-170-24 36 72 8.1 450 4 US-08-029-170-24 37 72 8.1 627 1 US-08-295-814E-4 38 72 8.1 627 1 US-08-291-299-10 39 72 8.1 627 1 US-09-343-361-4 40 72 8.1 627 5 PCT-US93-01959-4 41 72 8.1 627 5 PCT-US93-01959-4 42 71 8.0 422 3 US-08-492-459-2 43 71 8.0 422 3 US-08-492-459-2 44 71 8.0 422 3 US-08-492-459-2 45 71 8.0 422 4 US-08-716-873-18
th 493;			Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 24, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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93 SIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLR 138

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                                                                                               Sequence 12, Application US/08928692 Patent No. 5958727
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Sequence 10, App11.
                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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         TITLE OF INVENTION:
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                                                                                                                                                                                  425 YIAELLGPY-VFIVFAVLLLLFFIFTFLKVPETKGRTFDEIAAAFR 469
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                             Local
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SOFTWARE: FastSEQ for Windows Version 2.0
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Meiklejohn, Ph.D., An.,
Meiklejohn, Ph.D., An.,
Mindber: 35,283
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                                  Lamsa, Michael
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Best Local :
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                       OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                   APPLICANT: Tartaglia, Louis A. APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC AC
                                                                                                                                                                                                                                           TITLE OF INVENTION:
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APPLICATION NUMBER: US/09/031,392 FILING DATE: 26-FEB-1998
                                                                           COMPUTER:
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REGISTRATION NUMBER: 33
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Pred. No. 7.4e-13;
0; Mismatches 49
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                                                                                                                                                                                                                                        USES THEREOF
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; MOLECULE TYPE: US-09-299-549-3
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Patent No. 6136547
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.9%; Score 176.5; DB 2
Best Local Similarity 33.3%; Pred. No. 9.3e-13;
Matches 40; Conservative 24; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM MEDIUM TYPE: Disketi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                               FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/299, FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tartaglia, Louis A. APPLICANT: Weng, Xun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 MSYLSIVAIFGEVAFFEVGPGPIPWFIVAELFSQGPRPAAIAVAGFSNWTSNFIVGNCFQ 314
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                                          TOPOLOGY:
                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                          LENGTH:
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                                                        : 383 amino acids amino acid
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1, Ph.D.,
35,283
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                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Diskett
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APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
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STREET: Boston
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                                                                  255 MSYLSIVAIFGFVAFFEVGPGPIPWFIVAELFSQGPRPAAIAVAGFSNWTSNFIVGMCFQ 314
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                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                     19 LVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVL 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & NATION STREET: 225 Franklin Street
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                                79 THWFMAFLYTKEENSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQIT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                        LENGTH:
SNWTSNFLVGLLFPSATFYLGAY-VFIVFTVFLVIFWVFTFFKVPETRGRTFEEIT 462
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                                                                                                                                                          19.9%; Score 176.5; DB 2 35.3%; Pred. No. 1.3e-12;
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                                                                                                                                       24; Mismatches
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US-09-299-549-5

; Sequence 5, Application US/09299549

Patent No. 6136547

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COMPUTER READABLE FORM:
                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  408
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                STREET:
CITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/0 FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    348 LMTISLLLKDNYSWMSFICIGAILVFVAFFEIGPGPIPWFIVAELFGQGPRPAAMAVAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                    19 LVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVL 78
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TOPOLOGY:
                                COUNTRY:
                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09 FILING DATE: 26-APR-1999
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SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                      SNWTSNFLVGLLFPSATFYLGAY-VFIVFTVFLVIFWVFTFFKVPETRGRTFEEIT 462
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             02110-2804
                                                              Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%; Score 176.5; DB 4 35.3%; Pred. No. 1.3e-12;
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                                                                                                                                          USES THEREOF
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US-09-299-549-6
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Best Local Similarity 32.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0:
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                       ALL.
STREET: L.
STREET: MOSTON
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REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                               OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 ELEYL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
              NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
                                                                                                                    APPLICATION NUMBER: FILING DATE: 26-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 YVAEAMGPY-VFLLFAVLLLGFFIFTFLRVPETRGRTFDQISAAFHRTPSLLEQEVKPST 498
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ELSWL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 MSYVSIVATFGFVAFFEIGPGPIPWFIVAELFSQGPRPAAMAVAGFSNWTSNFIIGMGFQ 439
                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 SIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDGPL--SVTGSP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 92
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                                                                                                                                                                                                                                                                                                                   225 Franklin Street
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SYSTEM: Windows95
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                                                                                 09/031,392
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                                                                                                                               US/09/299,549
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07334/072002
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Patent No. 5942398
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tartaglia APPLICANT: Weng, Xun TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                               MOLECULE TYPE:
                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                  FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                               TELEFAX: UTELEFAX: 200154
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                                                                                                                                                         TELEPHONE: 617/542-8906
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                                                                              TOPOLOGY:
                                                                                              TYPE:
                                                                                                                                                                                                                     REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/031,392
                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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STREET: 225 Franklin Street
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                                                                                                          LENGTH:
                                                                                                                                                                                                                                                 NAME: Meiklejohn, Ph.D.
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                                                                                                                                                                                                                                                                                                                                SYSTEM: Windows95 FastSEQ for Windows Version 2.0
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                                                            protein
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 19.2%;
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 Score 171;
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Length 534;
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                                                                                                                                  Matches
                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILLING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
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                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: GLUTEX AND USES THEREOF
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                                                                 391
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451 VAGFCNWACNFIVGMCFQYIADLCGPY-VFVVFAVLLLVFFLFAYLKVPETKGKSFEEIA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 ISAVAMTVGLVLLSQFAWMSYVSMVAIFLFVIFFEVGPGPIPWFIVAELFSQGPRPAAIA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                          TELEX:
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                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                 ISAEPADVHLGL----AWLAVGSMC---LFIAGFAVGMGPIPWLLMSEIFPLHIKGVATG 74
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                              VCVLTNWFMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQIT 134
                                                                 ISAVAMTVGLVLLSQFAWMSYVSMVAIFLFVIFFEVGPGPIPWFIVAELFSQGPRPAAIA 450
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                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                                                                                                  19.2%;
37.1%;
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                                                                                                                                  17; Mismatches
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                                                                                                                                                  Score 171; DB 4; Pred. No. 6.7e-12;
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                                                                                                                                                                  Length 534;
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OTHER INFORMATION:
US-08-355-844-3
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                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
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     477
                                 147 TGSPEL 152
                                                                                                                              364 MSYLSIVALFGEVAFFEVGPGPIPWFIVAELESQGPRPAAIAVAGFSNWTSNFIVGMCFQ 423
                                                                424 YVEQLCGPY-----VFIIFTVLLVLFFIRTYFKVPETKGRTFDEIASGFRQGGASQSD 476
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                                                                                                 93
                                                                                                                                                  33 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 92
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide LOCATION: 1..492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 30 Rock CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 14-DE
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                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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KTPEEL 482
                                                                                              SIMEILRPYGAFWLTAAFCILSVLETLTF-----VPETKGRTLEQITAHLRDGDGPLSV 146
                                                                                                                                                                                                 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 amino acids
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212-765-2519
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                                                                                                                                                                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                             18.5%; Score 164.5; DB 2 32.5%; Pred. No. 3.5e-11;
                                                                                                                                                                                                                                                                                         Facilitative glucose transportor Glutl protein
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                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                            DB 2;
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PCT-US95-16126-3
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                                                                                                                                                                                         Query Match
Best Local S
Matches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Tang, Henry Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 1..492 OTHER INFORMATION: OTHER INFORMATION:
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477 KTPEEL 482
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                                                                                                                                                         33 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 92
                                                                                                                                                                                         Local Similarity
hes 41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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                               TGSPEL 152
                                                              YVEQLCGPY-
                                                                                          SIMEILRPYGAFWLTAAFCILSVLFTLTF-----VPETKGRTLEQITAHLRDGDGPLSV 146
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10112-0228
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30 Rockefeller Plaza
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14-DEC-1994
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                                                              VFIIFTVLLVLFFIRTYFKVPETKGRTFDEIASGFRQGGASQSD 476
                                                                                                                                                                                       18.5%; Score 164.5; DB 5; 32.5%; Pred. No. 3.5e-11; 21ve 22; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A METHOD FOR PREDICTING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.5%; Score 164.5; DB 2 Best Local Similarity 32.7%; Pred. No. 4.5e-11; Matches 32; Conservative 21; Mismatches 44
                                                                                                                                                                     Patent No. 5958727
GENERAL INFORMATION:
                                                                                                                                                                                                            Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Patent No. 5
                                   APPLICANT: Brody, Howard
APPLICANT: Vaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modi
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
SECUENCE: COARACTERISTICS:
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APPLICANT:
                     CORRESPONDENCE ADDRESS
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                              STREET: 405 Lex
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                       512 TFAFFAGLSCLSTIFCYFCYPELSGLELEEVQTILKDG 549
                                                                                                                                                                                                                                                                                                                                           103 AFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDG 140
                                                                                                                                                                                                                                                                                                                                                                                                                   43 LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 584 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/928,692 FILING DATE: 12-SEPT-1997
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 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamsa, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
No. 5958727o No. 5958727disk of No. 5958727th America, Inc
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                                                                        Methods for Modifying the Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches 44;
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                                                                                                                                                                  Query Match 17.2%;
Best Local Similarity 33.7%;
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
432 QFFPMLNDLLGGRGKIYWIFAAMACLLGSFIYWWVPETKGK 472
                                                                         372 IYFNLKALSATAVLLFVASFAAGLGPVPFTLASELVGPEAVGAAQSWALGANWTATFTVA 431
                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 405 Le:
CITY: New York
                                 89 KEFNSIMEILRPYG-AFWLTAAFCILSVLFTLTFVPETKGR 128
                                                                                                             29 VHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVT 88
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                     TOPOLOGY:
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N: 435
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                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                    20; Mismatches 46; Indels 1;
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                                                                                                                                                                    Score 152.5; DB 2; Pred. No. 9.2e-10;
                                                                                                                                                                                    Length 488;
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1;

Search completed: February 13, 2002, 21:51:37 Job time: 6264 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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Maximum DB seq length: 2000000000
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PIR_68:*
1: pir1:*
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3: pir3:*
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889
1 WRPLZNZWIPRAAGIRHELV.....VTGSPELSWLRVSKGVEWPQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                   February 13, 2002, 21:53:10; Search time 79.58 Seconds (without alignments) 157.939 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match L	Length	DB	ID	Description
1	5 1	. 8	4	2	92	probable sugar tra
2	225	25.3	487	2	E96782	ical prot
ω			9	Ν	54	sugar
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6	204.5	ω.	$\vdash$	2	T12199	
7			$\sim$	ν	C84864	probable membrane
8	8	2	2	2	S12042	glucose transport
9	8	2	Ν	N	E86246	
10			9	2	A26430	ct
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ا ا د	۱ 🗗	- :	J 1	١ د	G86220	hypothetical prote
14		۳.	2	Ν	T10122	S
15	9	<del></del>	9	Ν	F96696	n F1N21.12
16	193.5	<del></del>	9	2	G85059	Œ
17	93.	1	æ	N	F71431	hypothetical prote
18	9	<u>-</u>	7	N	В86221	ical
19	9	۳.	9	2	T52132	ga
20	19	۳.	· w	2	H86340	Sugar transporter
21		μ,	w	N	S38435	hexose transport p
22	. 2	۲	œ	N	D86426	hypothetical prote
23	9	1	N	Ν	S06920	glucose transport
24	. 19	1.	7	N	S47089	Ų,
25			w	ы	S14144	hexose transport p
26	190	٠,	σ	Ν	в96829	Η,
27	190	21.4	7	2	в26430	ose isc
28	190	21.4	7	Ν	E85936	hypothetical prote
29	188.5	21.2	496	2	A31986	glucose transporte

## ALIGNMENTS

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metabolite transport protein homolog ywtG - Bacillus subtilis
C:Species: Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E70070
C:Accession: E70070
R:Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C:; Bron, S:; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Aro-266 1007
probable sugar transporter protein - beet C;Species: Beta vulgaris (beet) C;Date: 20-Sep_1999 #sequence_revision 20-Sep_1999 #text_change 21-Jul-2000 C;Accession: T14545 R;Chiou, T.J.; Bush, D.R. Plant Physiol 110, 511-520, 1996 A;Title: Molecular cloning, immunochemical localization to the vacuole, and A;Reference number: Z18131; MUID:96351183 A;Accession: T14545 A;Ccession: T14545
                                                                                                                                                                                                                                                                                                                                  Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Experimental source: tonoplast C:Superfamily: glucose transport | C:Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: 043629; NID: 91209755; PIDN: AAB53155.1; PID: 91209756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-490 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: F22H5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005173; NID:g10092276; PIDN:AAG12689.1; GSPDB:GN00141
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A; Status: preliminary
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                  447 LSWNSGGTFSIYMVVCAFTVAFVVIWVPETKGRTLEEI 484
                                                                                                                                                                                                                                                                                                                                                                                                388 LSVVGVVAMVVTFSLGIGAIPWIIMSEILPINIKGLAGSIATLANWFVAWIVTMTAN-IM
                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKBENSIM 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 IFPLHIKGVATGVCVLTINWFMAFLVTKEFNSIMEILRDYGAFWLTAAFCILSVLFTLTFV 122
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                                                                                                                                                                                                                                                                                                                                                          EILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 1.7e-12;
19; Mismatches 35;
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Pred. No. 1.4e-13;
0; Mismatches 48
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      S.; Galizzi,
Hosono, S.;
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                   A; Gene: T22H22.15
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-483 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A86141; MUID:21016719
A;Accession: D96589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T22H22.15 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: D9589
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C;Superfamily:
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A; Residues: 1-457 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15600.1; PID:g26361A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: E70070
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
427 WIISFTFNFLMN-WNPAGTFYVFATVCGATVIFVAKLVPETKGRTLEEI 474
                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 LMEAIGISYLFLIYAAIGIMAFLFVRFKVTETKGRSLEEIEQDLRDKNGQGGAAGKQQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 SWTTVICLGVFIVVFAVSWGPVVWVMLPELFPLHVRGIGTGVSTLMLHVGTLIVSLTYPI 395
                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 44; Conserv
                                FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI 133
                                                                                                                                EPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMA 84
                                                                                                  ESAGVSSKIGMIAMVVVQVYTGSFSLGMGGIPWVINSEIFPIDIKGSAGSLVTVVSWVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose transport protein
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE005173; NID:g3776581; PIDN:AAC64898.1; GSPDB:GN00141
                                                                                                                                                                                                                                           23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.8%;
                                                                                                                                                                                                                     25;
                                                                                                                                                                                                             Score 209.5; DB 2;
Pred. No. 4e-12;
25; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 212; DB 2;
Pred. No. 2.2e-12;
3; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 457
                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                            483;
                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.; White, (reasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                     426
                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.;
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RESULT 8
$12042
glucose transport
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                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 2
C:Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane transporter {imported} - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monosaccharid transport protein - fava bean
C:Species: Vicia faba (fava bean)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Jun-2000
                                                                                                                                      Вp
                                                                                                                                                                                                                                                                                  QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-521 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-516 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Weber, H.; Borisjuk, L.; Heim, U.; Sauer, N.; Wobus, U. Plant Cell 9, 895-908, 1997
A;Title: A role for sugar transporters during seed development: A:Reference number: Z17451; MUID:97355984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: At2g43330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002093; NID:g2289003; PIDN:AAB64332.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: G84864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G84864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: 293775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T12199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                      449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 FTFLVAQIFLTMLCHMK-FGLFLFFAFFVVVMTIYIYTMLPETKGIPIEEM 485
                                                                                                                                                                                                                                       389
                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 MAFLVTKEFNSIMETLRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGEPGDLPKWYAIVVVLFICIYVAGFAWSWGPLGWLVPSEIFPLEIRSAAQSVNVSVNML 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWF 82
                                                                                                                                   AEAAGTGMTFLILAGIAVLAVIFVIVFVPETQGLTFSEV
                                                                                                                                                                                 MEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI 133
                                                                                                                                                                                                                                  WLAVLGLALYIVFFAPGMGPVPWTVNSE1YPQQYRGICGGMSATVNWISNLIVAQTFLTI 448
                                                                                                                                                                                                                                                                                     WLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSI 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T12199
                                                                                                                                                                                                                                                                                                                                        Conservative
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  protein
     STP1
                                                                                                                                                                                                                                                                                                                                   22.7%; Score 202; DB 2; Length 521; 37.4%; Pred. No. 2.2e-11; tive 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.0%; Score 204.5; DB 2; 37.8%; Pred. No. 1.2e-11; tive 24; Mismatches 44;
  Arabidopsis
  thaliana
                                                                                                                                   487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecular characterizat
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                                                                                                                                                                                                                                                                                                                                           0
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  RESULT
A26430
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
DЬ
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                                                                                           В
                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                       C; Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-522 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A86141; MUID:21016719 A;Accession: E86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: E86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose transporter [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: glucose transport protein
C;Keywords: sugar transport; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X55350; NID: g16519; PIDN: CAA39037.1; PID: g16520 A; Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-522 < SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Primary structure, A;Reference number: S12042; A;Accession: S12042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Sauer, N.; Friedlaender, K.; Graeml-Wicke, EMBO J. 9, 3045-3050, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 24-Sep-1999
C:Accession: S12042; S14627
                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005172; NID: g5734730; PIDN: AAD49995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Theologis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E86246
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Best Local Similarity
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                           375
435 IFTFIIAQIFLTMLCHLK-FGLFLVFAFFVVVMSIFVYIFLPETKGIPIEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 VDGTPGELPKWYAIVVVTFICIYVAGFAWSWGPLGWLVPSEIFPLEIRSAAQSITVSVNM 434
                                            82
                                                                                                                                                                                  Local Similarity 33.9 nes 38; Conservative
                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 FMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW
                                                                                                                  FMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI
                                                                                           VDGTPGELPKWYAIVVVTFICIYVAGFAWSWGPLGWLVPSEIFPLEIRSAAQSITVSVNM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFTFIIAQIFLTMLCHLK-FGLFLVFAFFVVVMSIFVYIFLPETKGIPIEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.; Ecker, J.R.; Palm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                              22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%; Score 198.5; DB 2
33.9%; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic organization and MUID:91005995
                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                           Score 198.5; DB 2
Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                       45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Southwick, A.M.; Sun, Davis, R.W.
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                 Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485
                                                                                                                                                                                                                                                                                                                                                                                  GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Khaykin,
.S.; Maiti, R
                                                                                                                                                                                       1;
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n, E.;
R.; M
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Nucleic Acids Res. 16, 4097-4109, 1988
A:Title: 3'End of the malEFG operon in E.coli: localization of A:Reference number: S00776; MUID:88234001
A:Accession: S00874
A:Molecule type: DNA
A:Residues: 1-63,'V',65-192 <FRA>
A:Cross-references: EMBL:X06663; NID:g41953; PIDN:CAA29863.1; PC:Genetics:
A:Gene: xylE
A:Map position: 91.4
C:Superfamily: glucose transport protein
C:Keywords: transmembrane protein
                                                        B86096

xylose-proton symport [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-M.
C;Accession: B86096
C;Accession: B86096
C;Rerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pota
Nature 409, 529-533, 2001
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A; Residues: 1-491 <BLAT>
A; Cross-references: GB:AE000476; GB:U00096; NID:g1790456; PIDN:AAC77001.1; PID:g1790463
A; Experimental source: strain K-12, substrain MG1655
R; Francoz, E.; Dassa, E.
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R:Davis, E.O.; Henderson, P.J.F.
J. Biol. Chem. 262, 13928-13932, 1987
A:Title: The cloning and DNA sequence of the A:Reference number: A27418; MUID:88007632
A:Accession: A27418
A:Molecule type: DNA
A:Residues: 1491 <DAV>
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N;Alternate names: xylose-proton symport protein
C;Specles: Escherichia coli
C;Specles: Escherichia coli
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Sep-1999
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Sep-1999
C;Accession: A26430; A27418; F65210; S00874
R;Maiden, M.C.J.; Davis, E.O.; Baldwin, S.A.; Moore, D.C.M.; Henderson, P.J.
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: B86096
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.;
A; Rose, D.J.; Mau, B; Shao, Y.
Science 277, 1453-1462, 1997
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A; Residues: 1-491 <MAI>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGTAFYTQAPGIVALLSMLFYVAAFAMSWGPVCWVLLSEIFPNAIRGKALAIAVAAQWLA 418
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37.3%; Pr
tive 22;
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Pred. No. 5.4e-11;
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                                                                                                                                                                                                            16-Feb-2001 #text_change 31-Mar-2001
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                                                                                                                 J.D.; Rose, D.J.; Mayher Potamousis, K.; Apodaca
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A;Cross references: GB:AE005174; NID:g12518977; PIDN:AAG59230.1; GSPDB:GN00145; JWGP: A;Experimental source: Strain O157:H7, substrain EDL933
C;Genetics:
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A; Residues: 1-523 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1992 A; Description: A sink specific monosaccharid
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C; Superfamily:
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Best Local Similarity
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                                142 GPLSVTGSPELSWLRVSKGVEWP
                                                                                                                                            373 VNGTPGDLPKWYAIVVVIFTCVYVAGFAWSWGPLGWLVPSEIFPLEIRSAAQSINVSVNM
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                                                                                                                                                                              22 ISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                       .1 FTFIVAQVFLTMLCHLK - FGLFLFFAFFVVIMTVFIYFFLPETKNIPIEEMV
                                                                                                       FMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGD 141
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29.4%;
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Pred. No. 5.4
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Pred. No.
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. 9.8e-11;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ven

Venter, J.C.; Shinn, P.;

Davis, R.W.

Southwick,

A.M.;

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Tallo

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Khaykin, E Maiti, R.;

E.; Kim, ?.; Marzia

Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

R; Theologis, A.; Ecker, C; Accession: G86220

J.R.; Palm,

Conn, L.;

C.J.; Federspiel, Conway, A.B.; Conv

iel, N.A.; Kaul, Conway, A.R.; C

Creasy,

T.H.;

Dewar,

s.;

White,

O.; Alon

G86220

hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, A;Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-523 < MEII>
A; Cross-references: EMBL:LO8196; NID:g169717; PID:g169718
A; Experimental source: strain Carmencita; tissue-type coty
C; Genetics:
A; Gene: STC
C; Superfamily: glucose transport; transmembrane protein
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A;Accession: G86220
A;Status: preliminary
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A:Cross-references: GB:AE005172; NID:g2342688; PIDN:AAB70414.1;
C:Genetics:
A:Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein F1N21.12 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 002-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F96696
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A;Accession: T10122
A;Status: translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 194.5; DB 2
Pred. No. 1.1e-10;
                                                                                                                   C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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     Southwick, A.M.; Sun, H.;
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A;Map position: 1
C;Superfamily: glucose transport protein
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A; Residues: 1-493 <STO>
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A;Accession: F96696
                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: AEO05173; NID: g9828628;
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 40; Conserv
442 LFLRLLEKLGPRLLYSMFSTFCLMAVMFVKRNVIETKGKTLQEIEISL 489
                                         90 EFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHL 137
                                                                                                            30 HLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 89
                                                                                       HFSALCLSVGGTLVFVLTFALGAGPVPGLLLPEIFPSRIRAKAMAFCMSVHWVINFFVGL 441
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Q01440 leishmania
P21906 zymomonas m
P54723 bacillus su
P13355 oryctolagus
P11167 rattus norv
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P79365 ovis aries
P20303 sus scrofa
P27674 bos taurus
P11166 homo sapien
P17809 mus musculu
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P119357 rattus norv
P14672 homo sapien
P46896 gallus gall
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P87110 schizosacch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s E.O., Henderson P.J.F.;
cloning and DNA sequence of the gene xylE for xylose-proton
ort in Escherichia coli K12.";
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38; Conser
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Pred. No. 3.5e-10;
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PIR; S00874: S00874

EcoGene: EG11076; xylE.

InterPro; IPR003663; Sugar_trnsportr.

InterPro; IPR003663; Sugar_trnsportr.

Pfam; Pf00083; Sugar_tr; 1.

PRINTS; PR00171; STOGRTRNSPORT.
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CONFLICT
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PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar_transport; Transmembra
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EMBL; U00006; AAC43125.1; --
EMBL; AE000476; AAC77001.1; --
EMBL; AE005638; AAC59230.1; --
EMBL; AP002568; BAB38437.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88234001; PubMed=2836810;
Francoz E., Dassa E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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91
135
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77
111
155
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391
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465
           53608 MW;
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POTENTIAL.
A -> V (IN REF. 6).
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Tobe T.,
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Query Match Best Local Matches

Similarity

22.2%;

Conservative

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Score 197.5; DB Pred. No. 4e-10; 2; Mismatches

DB 1;

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15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
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PROSITE; PRO0216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
PROSITE; PS00217; SUGAR_TRANSPORT; Sugar transport;
POTENTIAL.
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Ricinus communis (Castor bean).

Ricinus communis (Castor bean).

Ricinus communis (Castor bean).

Ricinus communis (Castor bean).

Ricinus communis (Tracheophyta; Eukaryota; Enbryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosiderosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. CARMENCITA; TISSUE=Cotyledon; Weig A., Franz J., Sauer N., Komor E.; "Isolation of a family of cDNA-clones from Ricinus commu with close homology to the hexose carriers."; J. plant physiol. 143:178-183(1994).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PRO-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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                                                     ISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW 81
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L08191; AAA79764.1; -
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41; Conser
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Pred. No. 7.8e-10;
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074804EFA3A27F6B CRC64;
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P46333; O32289;
01-NOV-1995 (Re
15-JUL-1999 (Re
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MEDLINE-99303315; Pubmed-10376822;

Akbar S., Lee S.Y., Boylan S.A., Price C.W.;

Arbo genes from Bacillus subtilis under the sole cont
general stress transcription factor sigmaB.";

Microbiology 145:1069-1078(1999).

-i- FUNCTION: COULD SERVE EITHER A NUTRITIONAL OR AN
                   TRANSMEM TRANSMEM
                                                                                                                         TRANSMEM
TRANSMEM
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Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                            EMBL; AB005554; BAA21604.1; EMBL; Z99124; CAB16017.1; -SubtiList; BG11360; csbC.
                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.; "Cloning and sequencing of a 36-kb region of the Bacillus subtilis genome between the gnt and iol operons."; DNA Res. 2:61-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
15-JUL-1999 (Rel. 38, Last sanotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE METABOLITE TRANSPORT PROTEIN CSBC.
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CSBC_BACSU
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Kunst F., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujita Y., Shibayama Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168 / BGSC1A1;
MEDLINE=96093926; PubMed=7584049;
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                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PRO-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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the EMBL/GenB
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                                                                                                                                                                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hikawa H., Danchin
EMBL/GenBank/DDBJ
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                                                                                                                                                                         PROSITE; PS00216; SUGAR_TRANSPORT_1; 1. PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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                                                                                                                                                       Multigene
                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                 EMBL; X75440; CAA53192.1; -
                                                                                                                                                                                                                                                                                                                                                        Plant Physiol. 107:33-41(1995).
-!- FUNCTION: ACTIVE UPTAKE OF HEXOSES.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95175627; PubMed-7870840; Stadler R., Wolf K., Hilgarth C., Tanner W., Sauer N.K.; "Subcellular localization of the inducible Chlorella HUP1 monosaccharide-H+ symporter and cloning of a Co-induced galactose-H+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUP3_CHLKE
Q39525;
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Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella.
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Query Match

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Matches 42
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                                                                                                                      TRANSMEM
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InterPro; IPR003662; sub_trnsportr.
                                                                                                                                                                                                                                        EMBL; X79598; CAA56110.1;
                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 177:5379-5380(1995).

-!- FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing, and expression of the araE gene of Klebsiella oxytoca 8017, which encodes arabinose-H+ symport activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARAE_KLEOX
P45598;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95394866; PubMed=7665532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-8017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last annotation update)
ARABINOSE TRANSPORTER (ARABINOSE TRANSPORTER).
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01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
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                                                                                                                                                                                                     PF00083; sugar_tr;
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42; Conserv
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32, Last sequence update)
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8, Last annotation TRANS
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                                                                                                                                                   Transmembrane;
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                                                                                                                                        POTENTIAL.
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Pred. No. 1.2e-09;
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                                                                                                                                               Inner membrane; Symport.
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P15686; Q39523;
O1-APR-1990 (Rel. 14, Creat
15-JUL-1998 (Rel. 36, Last
15-JUL-1998 (Rel. 36, Last
H(+)/HEXOSE COTRANSPORTER 1
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PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane: Transport; Sugar transport;
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InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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                        TRANSMEM
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                                                                                                                                                                                                                                                                                      entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                       "The Chlorella H+/hexose cotransporter gene.";
Curr. Genet. 19:215-219(1991).
-!- FUNCTION: ACTIVE UPTAKE OF HEXOSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE#91330335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cotransporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90092536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chiorella.
NCBI_TaxID=3074;
           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                            K., Tanner W.,
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Last annotation update)
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ches 53;
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Best Local Similarity
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CONFLICT
CONFLICT
SEQUENCE
                                                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., Rc Gregor J., Davis N.W., Kirkpatrick H.A., Gos Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARAE_ECOLI STANDARD; PRT; 4

P09830; Q46937;

01-MAR-1989 (Rel. 10, Created)

01-MAR-1989 (Rel. 10, Last sequence up

20-AUG-2001 (Rel. 40, Last annotation a

ARAE OR B2841 OR Z4161 OR ECS3698.
                         Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / JW2433;
MEDILINE=88228015; PubMed=2836407;
Maiden M.C.J., Jones-Mortimer M.C., Henderson P.J.F.;
"The cloning, DNA sequence, and overexpression of the gene araE coding for arabinose-proton symport in Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87115869; PubMed=3543693;
Maiden M.C.J., Davis E.O., Baldwin
Henderson P.J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli, and
Escherichia coli O157:H7.
Bacteria; Proteobacteria;
STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                               STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=0157:H7 / E
                                                                                                                                                                                                                   "The
                                                                                                                                                                                                                                                                                STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                          J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mammalian and bacterial sugar transport Nature 325:641-643(1987).
              SEQUENCE FROM N.A.
                                                                                                                                                                                                      Science
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                                                                                                                                                                                                     complete genome sequence nce 277:1453-1474(1997).
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57522 MW;
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Pred. No. 1.
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TRANSPORTER).
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PROSITE; PS00216; SUGAR_TRNSPORT_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. MOL. BIOL. 171:369-381(1983).
-I- FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE WITH THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B26430; B26430.
PIR; A28075; A28075.
EcoGene; EG10056; araE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The araE low affinity L-arabinose transport promoter. Cloning, sequence, transcription start site and DNA binding sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE005513; EMBL; AP002563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY SEQUENCE OF 1-28 FROM N.A. MEDLINE=84114868; PubMed=6319708; Stoner C., Schleif R.F.;
                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                Complete
                                                                                                                                                                                                                                                                                                                                                             Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21156231; PubMed=11258796;
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                       NSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGD 141
                                                                          GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEF 91
LTLLDSIGAAGTFWLYTALNIAFVGITFWLIPETKNVTLEHIERKLMAGE 465
                                                  GLSWLSVGMTMMCIAGYAMSAAPVVWILCSEIQPLKCRDFGITCSTTTNWVSNMIIGATF
                                                                                                                                                                                                                                                                                                                                                                                                                PF00083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X00272;
U29581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE000368; AAC75880.1; -. AE005513; AAG57953.1; -. AP002563; BAB37121.1; -.
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                                                                                                               Similarity
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t; Sugar transport;
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                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA23469.1;
                                                                                                                                                                                                                                                                                                                                                                                                sugar_tr; 1.
1; SUGRTRNSPORT
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Pred. No. 1
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411990A441D44393 CRC64;
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GTR2_MOUS 9
GTR2_MOUSE
ID GTR2_MOUSE
AC P14246;
DT 01-FB-1996
DT 01-FB-1996
DT 01-NOV-1997
DE GLUCOSE TRAIGN SLC2A2 OR GIO
OS MUS MUSCULUS
CO MAMMABILINE=9000
RA SUZUE K. L.
RY SEQUENCE FR
RC STRAIN=BALB
RX MEDLINE=9000
RA SUZUE K. L.
RT "Sequence of
RL (2)
RY MEDLINE=9000
RA SUZUE K. L.
RT "SEQUENCE FR
RP SEQUENCE FR
R
                                                                                       EMBL; X16986; EMBL; X15684; EMBL; S77926;
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MEDLINE=92111400; PubMed=1765007;
Hogan A., Heyner S., Charron M.J., Copeland N.G., Gilbert D.J.
Jenkins N.A., Thorens B., Schultz G.A.;
"Glucose transporter gene expression in early mouse embryos.";
Development 113:363-372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE-Liver;
MEDLINE=8936666; PubMed=2771649;
Asano T., Shibasaki Y., Lin J.L., Akanu
"The nuclectide sequence of cDNA for a
transporter protein";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
GLUCOSE TRANSPORTER TYPE 2, LIVER.
                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                entities requires a license agreement (See
                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            postimplantation mouse embryos.";
Development 116:555-561(1992).
-!- FUNCTION: FACILITATIVE GLUCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Differential screening of a PCR-generated mouse embryo cDNA library: glucose transporters are differentially expressed in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93170163; PubMed=1289053;
Smith D.E., Gridley T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suzue K., Lodish H.F., Thorens B.; "Sequence of the mouse liver glucose transporter."; Nucleic Acids Res. 17:10099-10099(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUE=Liver; MEDLINE=90098776; PubMed=2602116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSPER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HEPATOCYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; IT MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. IT MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE & KIDNEY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN ENDODERM LAYER OF YOLK SAC AND LIVER PRIMORDIUM.
                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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; CAA33719.1;
; AAB20847.1;
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\$06920; \$06920. \$05319; \$05319.

MGI:1095438; Slc2a2

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RESULT 10
GTR3_HUMAN
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Best Local 9
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Bell G.I.;
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Evidence for a family of human glucc
"Evidence for a family of human glucc
Sequence and gene localization of a property of the sequence of a family of the sequence of a family of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequen
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P1116;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
GLUCOSE TRANSPORTER TYPE 3, BRAIN.
SLC2A3 OR GLUT3.
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Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR01191; GLUCTRSPORT2.
                                                  J. Biol. Chem. 263:15245-15248(1988-i- FUNCTION: FACILITATIVE GLUCOSE
                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89008414;
                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS00217; SUGAR_TRANSPORT_2;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE TISSUE SPECIFICITY: HIGHLY EXPRESSED IN
                                     GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDG
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                                                                                                                                                            T., Fukumoto
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IPR003662;
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                                                                                                                                                            Eddy
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N-LINKED (GLCNAC. . .) (POT
G -> D (IN REF. 2).

N -> T (IN REF. 2).

S -> T (IN REF. 2).

S -> F (IN REF. 2).

L -> F (IN REF. 1).

P -> S (IN REF. 1).
                                                                                                                                                            R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 190;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                          glucose
                                                  TRANSPORTER. PROBABLY
                                                                                                                                                            Fan Y.-S.,
                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                        transporter-like
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.9e-09;
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                                                                                                                                                                                                                                                      Hominidae; Homo
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 BRAIN
                  PROTEIN
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                                                                                                                                                            M.G.,
                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                         in
                                                                                                       proteins.
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                                                      NEURONAL
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                 GTR2_RAT STANDARD: PRT; 5
P12336;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
GLUCOSE TRANSPORTER TYPE 2, LIVER.
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TRANSMEM
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TRANSMEM
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InterPro: IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
PRINTS: PR00171; SUGATRNSPORT.
PRINTS: PR00172; GLUCTRNSPORT.
PRINTS; PR00172; GLUCTRSPORT3.
PRINTS; PR00192; GLUCTRSPORT3.
                                          SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A31986; A31986
MIM; 138170; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
NCBI_TaxID=10116;
            Mammalia; Eutheria; Rodentia;
                     Eukaryota; Metazoa;
                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                 --AHLRDGDG
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                                                                                                                                                                                                      SNWTSNFLVGLLFPSAAHYLGAY-VFIIFTGFLITFLAFTFFKVPETRGRTFEDITRAFE
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                      Chordata;
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POTENTIAL.
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            Sciurognathi;
                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                              F601CD6892F16516 CRC64;
                                                                                                                                                                                                                                                                                          Mismatches
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No. 2.
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             Muridae; Murinae; Rattus.
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MBL outstation -
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Best Local Similarity
Matches 42; Conser
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TRANSMEM 11
DOMAIN 32
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TRANSMEM 126
TRANSMEM 157
TRANSMEM 157
TRANSMEM 186
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SEQUENCE
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TRANSMEM
TRANSMEM
             443 VCNFIIALCFQYIADFLGPY-VFFLFAGVVLVFTLFTFFKVPETKGKSFDEIAAEFRKKS
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                                                                             383
                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00216; SUGAR_TRANSPORT_1; PROSITE; PS00217; SUGAR_TRANSPORT_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00172; PRINTS; PR01191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                               82 FMAFLVTKEFNSIMEILRPYGÄFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGD 141
                                                                                         31 LGL-----AWLAVGSMC---LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
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Cell 5
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MEDLINE-89003066; Pubmed-3048704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Thorens B., Sarkar H.K., Kaback H.R., Lodish H.F.,
"Cloning and functional expression in bacteria of a novel glucose
transporter present in liver, intestine, kidney, and beta-pancreatic
islet cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA THE BETA CELLS; IT MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. IT MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE & KIDNEY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: PRESENT IN LIVER, INTESTINE, KIDNEY AND BETA-PANCREATIC ISLET CELLS.

SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
                                                                  LGLVLLDKFTWMSYVSMTAIFLFVSFFEIGPGPIPWFMVAEFFSQGPRPTALALAAFSNW
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                                                                                                                           Conservative
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460
481
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Pred. No. 5.2e-09;
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CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                         48;
                                                                                                                                               Length 522;
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                                                                                                                                                                                                  (POTENTIAL)
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Query Match
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InterPro; IPR003662; sub_trnsportr.
Pfam; Pf00083; sugar_tr_I
PRINTS; PR00171; SUGRTRNSPORT_I,
PROSITE; PS00216; SUGAR_TRANSPORT_I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG12148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000377; AAC75980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U28377; AAA69110.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INN
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9742661; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: UPTAKE OF GALACTOSE ACROSS THE BOUNDARY MEMBRANE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALP_ECOLI P37021;
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01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GALACTOSE-PROTON SYMPORTER (GALACTOSE TRANSPORTER).
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01-JUN-1994
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PS00217; SUGAR_TRANSPORT_2; 1.
PS00217; SUGAR_TRANSPORT; Transmembrane;
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      Score 184.5; DB 1;
Pred. No. 5.1e-09;
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01-FEB-1996 (Rel.
15-JUL-1999 (Rel.
                                                                                                                               TRANSMEM TRANSMEM
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"Canine brain glucose transporter 3: gene seq
comparisons and analysis of functional sites.
Gene 16:251-256(1996).
-i- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                           TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00171; SUGRTRNSPORT. PRINTS; PR00172; GLUCTRNSPORT. PRINTS; PR01192; GLUCTRSPORT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collable ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions European Formatics institutions as long as its content is in by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCOSE TRANSPORTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR003663; Sugar_trnsportr.
Pro; IPR003662; sub_trnsportr.
PF00083; Sugar_tr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Best Local
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01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
01-NOV-1997 (Rel. 3
                                  EMBL;
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EMBL;
EMBL;
                                                                                             EMBL;
                                                                                                                                                     modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                              Takeda J., Minokoshi Y., Yas
Submitted (JUL-1994) to the
                                                                                                                                                                                                                                                                                                                                                              GLUT3, the brain facilitative glucose transporter isoform, and identification of sites of expression by in situ hybridization."; J. Biol. Chem. 267:467-472(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92112695; PubMed=1730609; Nagamatsu S., Kornhauser J.M., Seino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTR3_MOUSE
                                                                                                         EMBL;
                                                                                                                     EMBL;
                                                                                                                                              or send an
                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                       between
                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC2A3 OR GLUT3 OR GLUT-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUCOSE TRANSPORTER
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                                                                                                                                                                                                                                                                                                                                                                                                             Bell G
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                "Glucose transporter expression in brain. cDNA sequence of mouse
                                                                                                                                                                                                                                                                                                                                                   2
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                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                        GLUCOSE TRANSPORTER
                                                                                                                                                                                                                                                                                                   FUNCTION: FACILITATIVE GLUCOSE
M75135; X61093; U11854; U11845; U11846; U11848; U11849; U11850; U11852;
                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb|LMTTSLLLKDNYNWMSFVCTGAILVFVAFFETGPGPTPWFTVAELFSQGPRPAAMAVAGC|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                              non-profit institutions as long
                                                                                                                                           equires a license agreement (See http://www.isb-sib.email to license@isb-sib.ch).
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AAB60666.1;
AAB60666.1;
AAB60666.1;
AAB60666.1;
AAB60666.1;
AAB60666.1;
AAB60666.1;
AAB60666.1;
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AAB60666.
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26, Last sequence update)
35, Last annotation update)
ER TYPE 3, BRAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.5%;
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the EMBL/GenBank/DDBJ
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Pred. No. 9
                                                                                                                                                                    is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Sugar_trnsportr.

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RESULT 15
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Best Local
         TISSUE-Liver, and Kidney;

MEDLIND-88289735; PLDMed=3399500;

FUKUMOTO H., Seino S., Imura H., Sieno Y., Eddy R.L., FUKUShima Y.,

Byers M.G., Shows T.B., Bell G.I.;

Byers M.G., Shows T.B., Bell G.I.;

"Sequence, tissue distribution, and chromosomal localization of mRNA

"Sequence, tissue distribution, and chromosomal localization of mRNA

"Sequence, tissue distribution, and chromosomal localization of mRNA

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"Tissue distribution, and chromosomal localization of
                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCOSE TRANSPORTER TYPE 2, LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00171; SUGRTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PRINTS; PR01192; GLUCTRSPORT3.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                             SLC2A2 OR GLUT2
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PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A41751; A41751.
MGD; MGI:95757; Slc2a3.
InterPro; IPR003663; Sugar_trnsport
InterPro; IPR003662; Fig. trnsportr.
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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   MEDIATES
MEMBRANE
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Pred. No. 9.9e-09;
0; Mismatches 51;
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POTENTIAL.
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POTENTIAL.
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N-LINKED (GLCNAC. . .) (F
9090B8DCB8780082 CRC64;
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UPTAKE OF
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GLUCOSE
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                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00216; SUGAR_TRANSPORT_1; 1. PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J03810; AAA59514.1; -. PIR; A31318; A31318. MIM; 138160; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
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  454
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: LIVER, INSULIN-PRODUCING BETA CELL, SMAI INTESTIME, AND KIDNEY.
                                           FNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDG
FQYIADFCGPY-VFFLFAGVLLAFTLFTFFKVPETKGKSFEEIAAEFQKKSG
                                                                                            SWMSYVSMIAIFLFVSFFEIGPGPIPWFMVAEFFSQGPRPAALAIAAFSNWTCNFIVALC
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IPR003662; sub_trnsportr.
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34.8%;
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Search completed: February 13, Job time: 861 sec 2002, 22:06:05

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5: sp_invertebrate
6: sp_mammal:*
7: sp_mtc:*
8: sp_organelle:*
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10: sp_plant:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		Query	on a t	7	<b>=</b>	
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	627	70.5	478	11	Q9JJZ1	Q9jjz1 rattus
N	627	70.5	479	11	Q9.JMA6	•
ω	590	66.4	477	11	Q9JJZ0	
4	585	65.8	477	1	Q9JJP4	Sum
5	585	65.8	477	11	Q9JIF3	mus
6	548	61.6	477	4	Q9NSC4	homo
7	540	60.7	477	4	Q9NY64	
80	282	31.7	507	4	Q9UGQ3	homo
9	278	31.3	433	σ	Q9V610	Q9v610 drosophila
10	271	30.5	489	U	094609	Q9v609 drosophila
11	268	30.1	463	10	Q9MAA4	Q9maa4 arabidopsis
12	262	29.5	539	σ	09VU17	Q9vul7 drosophila
13	257	28.9	348	10	Q9ZU87	Q9zu87 arabidops
14	248.5	28.0	465	ഗ	Q9V848	Q9v848 drosophila
15	239	26.9	444	ű	Q9V3G0	Q9v3g0 drosophila
16	232.5	26.2	621	0	Q9BE72	Q9be72 macaca fas
17	225	25.3	487	10	Q9FRL3	Q9frl3 arabidopsis
18	218.5	24.6	515	10	Q9LN48	Q9ln48 arabidopsis
19	213.5	24.0	490	10	039416	

45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20
191.5	192.5	192.5	192.5	193	193	193	193	193.5	193.5	194	194.5	194.5	194.5	195	197	198.5	199.5	201	202	204.5	206.5	207	208.5	209.5	212
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497	580	519	339	734	734	496	474	582	461	493	510	492	378	523	581	522	491	558	521	516	501	477	510	483	457
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Q9VNJ1	Q9C757	Q9ZS76	Q9SCW6	Q9LM67	Q9SYQ3	065799	004036	023492	Q9M100	Q9FYG3	044827	044826	004040	Q06312	Q9LKH1	Q9SXB1	Q9VNJ2	Q9F1F2	022848	004078	Q9XHW3	Q9SCW9	065322	Q9ZVM0	P96742
Q9vnj1 drosophila	Q9c757 arabidopsis			Q91m67 arabidopsis		065 <b>7</b> 99 arabidopsis	004036 arabidopsis		Q9m100 arabidopsis	Q9fyg3 arabidopsis	O44827 caenorhabdi	O44826 caenorhabdi	004040 arabidopsis	Q06312 nicotiana t	Q91kh1 mesembryant	Q9sxb1 arabidopsis	Q9vnj2 drosophila	Q9fif2 arabidopsis	022848 arabidopsis	004078 vicia faba	Q9xhw3 oryza sativ	arabidop	065322 petunia hyb	Q9zvm0 arabidopsis	P96742 bacillus su

## ALIGNMENTS

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Ibberson M.R., Uldry M.A., Thorens B.;

"GLUTX1: A novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";

J. Biol. Chem. 275.4607-4612(2000).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL; AJ245936; CAB75719.1;

MGD; MGJ:1860103; GlutX1.

InterPro; IPR003662; sub_transporter.
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Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL; AB033418; BAA94383.1; --
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.

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Best Local Similarity
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-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; Y17802; CAB89815.1; -.
MGD: MG1:1860103; GlutX1.
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003663; Sugar_transporter.
PFam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGATRNSPORT_1; UNKNOWN_2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JJP4;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003663; Sugar_transporter.
pfam; pF00083; sugar_tr; 1.
PRINTS; pR00171; SUGATRNSPORT.
pROSITE; pS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
pROSITE; pS00217; SUGAR_TRANSPORT_2; 1.
 Q9JIF3
                                                                                                                                                                                                                                                                                                                                             Transmembrane. SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose transport activity.";
J. Biol. Chem. 275:16275-16280(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane. SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doege H., Schuermann A., Bahrenberg "GLUT8: A novel member of the sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUTX1 OR GLUT8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20283667; PubMed=10821868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 TNWFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCALSVLFTLTVVPETKGRTLEQVTAH
                                                                                                                                                                       356 LYPIAAEPYDVQVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 LVPTAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVL 415
                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVL
                                      ú
                                                                                                                                  TNWFMAFLYTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAH
                                                                                                                                                                                         TNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCALSVLFTLTVVPETKGRTLEQVTAH
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s (Mouse).
Metazoa; Chordata; C
                                                                                                                                                                                                                                                   Conservative
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 PRELIMINARY;
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89.8%;
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90.78;
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Pred. No. 4.9e-47;
                                                                                                                                                                                                                                                                   Score 585; DB 11;
Pred. No. 1.4e-46;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Length 477;

(BY

SIMILARITY)

H.G.; family

with

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Best Local Similarity
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O9NSC4;
O1-OCT-2000 (TrEMBLrel. 1:
O1-OCT-2000 (TrEMBLrel. 1:
O1-JUN-2001 (TrEMBLrel. 1:
O1-JUN-2001 (TrEMBLRel. 1:
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EMBL; AF232061; AAF78366.1; -.
     InterPro;
Pfam; PF0
                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUT8
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InterPro; IPR003663; sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTENSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                    InterPro; IPR003662; sub_transporter
InterPro; IPR003663; Sugar_transporter
                                                                                                                                                                                                                                               MEDLINE=20283667; PubMed=10821868;
                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCOSE TRANSPORTER GLUT8.
                                                                                                                                                                                               Doege H., Schuermann A., Bahrenberg C., Brauers A., Joost "GLUT8: A novel member of the sugar transport facilitator
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVL 415
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                                                                                                                                                                                                                                                                                                                                                                       Primates;
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89.8%;
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Last annotation update)
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Pred. No. 1.
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                                                                                                                          MEMBRANE PROTEIN
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l.4e-46;
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                                                                                                                                                                                               Joost H.G.;
itator family with
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                                                                                                                          SIMILARITY)
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 Q9UGQ3;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, GITCOCCE TREASCONTERNS
                                                                                                                                                                                                                                                                                                                                                                               "GLUTX1: A novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues.";
J. Biol. Chem. 275:4607-4612(2000).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY:
-i- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AJ245937; CAB75702.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane. sequence 477 AA;
                                                                                                                                                                                                                                                                                                                              Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
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01-OCT-2000
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                                                  090603
                                                                                                                                                                                                                                                                                SEQUENCE
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003662; sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ibberson M.R., Uldry M.A., Thorens B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20138191; PubMed=10671487;
                                                                                                                 418
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                                                                                                              21 PISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTN
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97; Conser
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;; PS00216; SUGAR_TRANSPORT_1;
;; PS00217; SUGAR_TRANSPORT_2;
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(TrEMBLrel.) (TrEMBLrel.
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82.8%;
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83.6%;
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Pred. No. 2.
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Best Local :
MEDLINE-2019606; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                      STRAIN-BERKELEY;
                                                                                                                                                                                                                                  SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG8234 PROTEIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT_2; 1.
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"Activity and genomic organization of human glucose transporter 9
(GLUT9), a novel member of the family of sugar-transport facilitators
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AJ011372; CAB66155.1;
-- EMBL; Y17803; CAB66155.1;
-- EMBL; Y17803; CAB69996.1;
-- TENCACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 CVPETKGRSLEQIESFFRMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPLSPN---STAGLESESWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPITWLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPLZNZWIPRAAGIRHELVPISAEPADVHLG-LAWLAVGSMCLFIAGFAVGWGPIPWLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (Human)
ryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Woodward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sugar transporter gene, a G-beta subunit
enes in human chromosome 9q34 ";
P-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 282; DB 4;
Pred. No. 2.6e-18;
22; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aziz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1FC6E2EB11588460 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burley M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit like
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                                                                                                                                                                                                                                                                                                                                                     Muscomorpha
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               S.N.
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Q9V609
ID QS
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DT 01
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DT 01
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                                             RESULT
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                                                                                                                                                                                    Matches
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Best Local
  Q9V609;
Q9V609;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                            InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGARMSPORT_1; 2.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                  Transmembrane.
                                                                  419
                                                                               143
                                                                                                                                                                                                                                       FlyBase; FBgn0033644; CG8234
                                                                                       360 CTFVVTKTFQDLTVAMGAHGAFWLFGAICIVGLFFVIIFVPETRGKSLEEIERKMM-GRV 418
                                                                                                                        302
                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe I Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C
                                                                                                                                     24
                                             10
                                                                               PLS
                                                                 PMS
                                                                                                    MAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDG
                                                                                                                         AEPADV-HLGLAWLAVGSMCLETAGFAVGWGPIPWLLMSBIFPLHIKGVATGVCVLTNWF
                                                                                                                   AHGPDVSHLG--WLPLTCFVIYILGFSLGFGPIPWLMMGEILPAKIRGPAASVVTAFNWF
                                                                                                                                                  l Similarity
55; Conser
                                                                               145
 ) (TrEMBLrel. 13, 13) (TrEMBLrel. 13, 15) (TrEMBLrel. 17, 17)
                             PRELIMINARY;
                                                                                                                                                 Conservative
                                                                                                                                                                                   AA;
                                                                                                                                                                                  47357 MW;
                                                                                                                                                       31.3%;
44.7%;
                                                                                                                                                21;
              Created)
Last sequence up
                                                                                                                                               Score 278; DB 5;
Pred. No. 5.1e-18;
1; Mismatches 4;
                             PRT;
                                                                                                                                                                               63F0E13046A769DD CRC64;
                            489
       update)
update)
                                                                                                                                               43;
                                                                                                                                                           Length 433
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chandra I.,
                                                                                                                                              4.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                    H.O.,
                                                                                                                  359
                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                        K.A.,
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422 TFQDLTVAMGAHGAFWLFGAICFVGLFFVIIYVPETQGKTLEDI 465

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIson C.M., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHalov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA McHalov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA McHalov G., Mishina N.V., Mobarry C., Morris J., McShrefi A.,
RA Ralaczlo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ralaczlo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ralaczlo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong W., Zhong S., Yao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
RC C. --- Sulfia H.G. Zharion - Thergran Membane Deoretin (By Sintil Apiron)
                                                                                                                                                                                       Matches
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Ways A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Quan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preitfer Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG7801
CG7801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abril J.F., A
Ballew R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00216; SUGAR_TRANSPORT_1; PROSITE: PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0033643; CG7801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003662; sub_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY EMBL; AE003825; AAF58631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                 364
                              90
EFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQI
                                                                            HLG--WLPLTCFVIYILGFSLGFGPIPWLMMGEILPAKIRGSAASVATAFNWFCTFVVTK 42
                                                                                                                                HLGLAWLAVGSMCLFTAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 89
                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003663; Sugar_transporter
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                    53026 MW;
                                                                                                                                                                                                       30.5%; Score 271; DB 5;
46.2%; Pred. No. 2.6e-17;
                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                    D26436DAD69723C6 CRC64;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Champe M., Pfeiffer B.D.,
                                                                                                                                                                                       36;
                                                                                                                                                                                                                                     Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gocayne J.D.,
A., Galle R.F.,
Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iklos G.L.G.,
Baldwin D.,
                                                                                                                                                                                    Gaps
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Best Local
                                                                                                                                                                    Q9VU17
Q9VU17;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MAA4;
Q9MAA4;
01·OCT-2000
01·OCT-2000
01·JUN-2001
                                                                                              Eukaryota; Metazoa; Pterygota; Neoptera;
                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                           CG10960 PROTEIN.
CG10960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M., "Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A.,
                              STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Sugar transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE SUGAR TRANSPORTER
                                            SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=7227;
                                                                                        Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY
EMBL; AC009177; AAF27021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
                                                                                                                                                                                                                                                                                                  451
                                                                                                                                                                                                                                                                                                                             126
                                                                                                                                                                                                                                                                                                                                                                                                               345
                                                                                                                                                                                                                                                                                                                                                         392 INLKGTAGGLVTVVNWLSSWLVSFTFNFLM-IWSPHGTFYVYGGVCVLAIIFIAKLVPET
                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                           KGRTLEQITA 135
                                                                                                                                                                                                                                                                                                                                                                                LHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPET 125
                                                                                                                                                                                                                                                                                                                                                                                                              NSFLLKAHGLALDIIPA------LAVSGVLVYIGSFSIGMGAIPWVIMSEIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                         NZWIPRAAGIRHELVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFP
                                                                                                                                                                                                                                                                                                  KGRTLEEIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMBIA;
                                                                                                                                                                     (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                   Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.1%;
38.5%;
                                                                                   Endopterygota; Diptera; ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82B93947AE79DAC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268;
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                                                                                                                                                                                                                               539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; DB 10;
. 4.7e-17;
 Evans C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
  Gocayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                391
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RESULT
Q9ZU87
ID Q9
AC Q9
DT 01
DT 01
DT 01
DF PI
GN T'
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                                                                                                                                                                                                                                                                                                                                                                  Qy
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"The genome seguence of Drosophila melanogaster.";

CC. "SUBCELULAR LOCATION. INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                    Q9ZU87

Q9ZU87;

Q9ZU87;

Q9ZU87;

Q1-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-JUN-2001 (TrEMBLrel. 17, L
PUTATIVE SUGAR TRANSPORTER.
    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003540; AAF49874.1; FlyBase; FB9n0033316; CG10960.
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS: PR00171; SUGETRNSPORT.
                                                                                                                                                                                                                                                                                                           419 VSLGWLPVASLCLFIIMFSIGYGPVPWLMMGELFATDIKGFAGSLAGTSNWLLAFVVTKT
                                                                                                                                                                                                                                                   479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                         91 FNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHL 137
                                                                                                                                                                                                                                                                                                                                                 31 LGLAWLAVGSMCLFIAGFAVGWGFIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKE 90
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                FVNLNDGLGIGGTFWLFAGLTVVGVIFVYFAVPETKGKSLNEIQQEL 525
                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58413 MW;
(Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                         29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                  Last sequence update)
Last annotation update)
                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 262; DB 5
Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2F4814DBF676BBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                       348
                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 539
                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RC STRAIN=BERKELEX;

RX MEDILINE=2019606; PubMed=10731132;

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Wan, K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan, K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Basson K.Y., Benos P.V., Berman B.P., Bayraktaroglu L., Beasley E.M.,
RA Boskova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
RA Boskova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
                                                            ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMPAGNATION ACCOMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
MEDLINE->>>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG6484 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9V848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9V848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E., Barnstead M.E., Wason T.M., Bowman C.L., Ronning C.M., Benito M., Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C., Fraser C.M., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence.", Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 TLVNWFGAWAVSYTENELMS-WSSYGTFLIYAAINALAIVFVIAIVPETKGKTLEQIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugar transport; Transmembrane. SEQUENCE 348 AA; 36899 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003662; sub_transporter. Pfam; PF00083; sugar_tr; 1. PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AC006072; AAD13706.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 HEAVPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 VLTNWFMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEOITA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 HELVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Meoptera; Endopterygota; Diptera; Brachycera; Musca; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LAVVGIMVYIGSFSAGMGAMPWVVMSEIFPINIKGVAGGMA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13, Created)13, Last sequence update)17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erygota; Diptera; Brachycera; Muscomorpha; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 257; DB 10;
Pred. No. 3.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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RESULT 15
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ID 993G0
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Shorg E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Best Local
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V3G0;
                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Phannoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUT4 PROTEIN.
SUT4 OR CG1380
      Ballew R.M.,
Beeson K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS: PR00171; SUGRTRNSPORT.

PROSITE: PS00216; SUGAR_TRANSPORT_1;
PROSITE: PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-i- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AE003802; AAF57829.1; -
FlyBase; FBgn0034247; CG6484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPher
                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
SEQUENCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHLRDGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVVTLLFPILKSSIGPGPTFWIFTAIAVIAFFYSLFFVPETKGKTIIEIQDLLSGGKG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPASMD-NFGWLPISSICIFIIFFSIGFGPVPWLVMAELFSEDVKSVAGSIAGTSNWLSA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 38.1
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Na; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.0%;
38.1%;
   Berman B.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 248.5; DB 5
Pred. No. 3.1e-15;
7; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             004B4CACF406BDBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
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Liang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
   Bolshakov
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Search completed: February 13, Job time: 864 sec

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegvam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupskim M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rublin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.*;
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                    Query Match
Best Local :
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY S-1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AE003831; AAF58847.1; -.
EMBL; AF199486; AAF13274.1; -.
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT; Transmembrane.
SEQUENCE 444 AA; 48028 MW; D1806845
                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0028560; sut4.
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cl
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P
Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                              334
394 PVLNDIIGATACFAIFFGFAVAAFVFILFLIPETKGKTLNEIQAKM 439
                                                                                                                                                                                                                    Local Similarity
                                                92
                                                                                                                     GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEF
                                                NSIMEILRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHL 137
                                                                                              GVGWLALIAVCVFIIGESLGFGPVPWLMMAELFAEDVKALAGSIAGTTNWCFAFIVTLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botchan M.R.,
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Busam D.A., Butler H.,
                                                                                                                                                                                                                    26.9%;
39.6%;
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                                                                                                                                                                                                                    Score 239; DB 5;
Pred. No. 2.2e-14;
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Page 8

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Result
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### ALIGNMENTS

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AAB66933 standard; Protein;

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AAB66933;

Rat GLUTX1. 17-APR-2001

(first entry)

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14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                                                                 Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
        N-PSDB; AAF55866
                WPI; 2001-112615/12
                                 Thorens B,
                                                                                                              14-JUL-2000; 2000WO-IB01042
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Best Local S
Matches 94
                               Claim 11; Page 74-75; 124pp; English
                                                          Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                                WPI;
                                                                                                                                        Thorens
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27-AUG-1999;
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The present invention re AAB66932-AAB66941): The

relates

GLUTX

to GLUTX

proteins (AAF55865-AAF55871 are related to the facultat

and

Sequence

477

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is murine GLUTX1.

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RESULT
AAB66934
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Best Local
                                                                                                                                                                                                                                                                      14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
                                                                                                          Claim 11; Page 73-74; 124pp; English
                                                                                                                                  e.g. ischemia and diabetes
                                                                                                                                              the
                                                                                                                                                                                          WPI; 2001-112615/12.
                                                                                                                                                         Nucleic acids encoding
                                                                                                                                                                                N-PSDB; AAF55867
                                                                                                                                                                                                                                     (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                             13-JUL-2000;
                                                                                                                                                                                                                                                                                                                   14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66934 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                        hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                Murine; GLUTX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB66934;
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                                                                                                                                                                                                                                                                                                                                                                                                                     hexose transport
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                                                                                                                                             prevention, diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
87; Conserv
                                                                                                                                                                                                                В,
                                                                                                                                                                                                                                                                     99US-0143907.
99US-0151140.
2000US-0184285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA;
                                                                                                                                                                                                                Ibberson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                   2000WO-IB01042
                                                                                                                                                                                                                                                            2000US-0616132
                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; vaccine; hexose transport modulator;
rt disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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92.68;
                                                                                                                                        GLUTX glucose transporter proteins, useful in sis and treatment of hexose transport disorders,
                                                                                                                                                                                                               Uldry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
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Best Local
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                                                                                                            14-JAN-2000; 2000US-0176083
21-JAN-2000; 2000US-0177332
28-JAN-2000; 2000US-0178572
02-FEB-2000; 2000US-0179758
10-FEB-2000; 2000US-0181625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       demyelinating disease; mental disorder; Schizophrenia; polymyositis;
muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
                                                                                                                                                                                                                                                     WO200146258-A2
                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        malabsorption syndrome; hypercholesterolaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human transporter and ion channel-1 (TRICH-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE04888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE04888 standard;
                                                                                                                                                                                                    22-DEC-2000; 2000WO-US35095
                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-2001
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 2001-418042/44
DB; AAD09552.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epvdvqvglawlavgsmclfiagfavgwgpipwllmseifplhvkgvatgicvltnwfma 42
                          Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                             MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis
                                                                                     INCYTE
                                                            Burford N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                               Azimzai
                                                                                     GENOMICS
                                                                                                                                                                           99US-0172000
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 29..474
                                                                                                                                                                                                                                                                                           438..457
                                                                                                                                                                                                                                                                            /label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                   . 339
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                                                                                                                                                                                                                                                                                                                                                                               "Sugar transporter domain"
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                                              Au-Young J, Lu
Yue H, Nguyen
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                                               DAM,
                                               Yang J,
Yao MG,
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                                                            Reddy
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14-JUL-1999; 27-AUG-1999; 23-FEB-2000; 13-JUL-2000;

99US-0143907. 99US-0151140. 2000US-0184285. 2000US-0616132.

14-JUL-2000;

2000WO-IB01042

18-JAN-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, ammesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
                                                                                                                                                                                                                                           Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                            Human GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human transporter an and preventing transport,
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                            17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 112-113; 160pp;
                                                                                                                                                          WO200104145-A2
                                                                                                                                                                                                                          hypoglycaemia;
                                                                                                                                                                                                                          hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                            AAB66932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRICH is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422
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                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transporter and ion channel proteins useful for treating ing transport, neurological, muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as vaccine.
                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transporter and ion channel-1 (TRICH-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRICH is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 457; DB 22; Pred. No. 3.3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT
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                                                      25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
23-AUG-1999;
                                                                                                  24-AUG-1998;
24-AUG-1998;
09-SEP-1998;
28-SEP-1998;
                                                                                                                                                                                                                                                      Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflam infection; fungal, bacterial; viral; HTV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive.
                                                                                                                                                                                    02-MAR-2000
                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                Human secreted
                                                                                                                                                                                                                                                                                                                                                              AAY95019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT3-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is human GLUTX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 70-71; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders
                                (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                            WO200011015-A1
                                                                                                                                                                                                                                                                                                                                       19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                    AAY95019 standard; Protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-112615/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                      98US-0113645.
98US-0113646.
99US-0379246.
                                                                                                                                                                                                                                                                                                               protein vq1_1,
                                                                                                   98US-0099618.
98US-0102092.
                                                                                                                          98US-0097638
98US-0097659
                                                                                                                                                             99WO-US19351
                                                                                          98US-0109978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 454; DB 22; I
pred. No. 7.9e-49;
""" amatches 6;
                                                                                                                                                                                                                                                                                                                SEQ ID
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                                                                                                                                                                                                                                                                                                                NO:78
                                                                                                                                                                                                                                                                                                                                                                                                                                            455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                              inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
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inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple solerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic
                                                                       lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; anti-inflammatory activity; and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-224657/19.
                                                    40 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Page 335-336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and cancer
  105
                                                    of the
  AA;
                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357pp; English
                                                                               one of the
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Matches
                                                                                                                                           Query Match
Best Local
                                                                                            19
                                                                                                                                          Local Similarity
62 pffffaaiclvslvft 77
                               79
                                                         LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 78
||| |:|||||| ||| :||| :| || ::
| fimgyavgwgpitwllmsevlplrargvasglcvlaswltafvltksflpvvstfglqv 61
                             AFWLTAAFCILSVLFT 94
                                                                                                                            39;
                                                                                                                           Conservative
                                                                                                                                        43.3%;
                                                                                                                           15;
                                                                                                                         Score 220; DB 21;
Pred. No. 3.6e-20;
5; Mismatches 22;
                                                                                                                                                        Length 105;
                                                                                                                           Indels
                                                                                                                           0;
                                                                                                                        Gaps
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δõ Ъ Ş

Вb

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RESULT
AAB45158
ID AAB4
AAB45158 standard; Protein;
                                               7
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Human secreted
                              12-FEB-2001
                                                            AAB45158;
                              (first entry)
protein sequence encoded by gene
                                                                                            106 AA
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opthalmalogical; autoimmorardiovascular disorder; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing; nervous system disorder; Human; secreted protein; immunosuppressive; antiarthritic; aging; antirheumatic;

39

SEQ ID

NO:99

Valenzuela D,

Yuan

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Hoffman

Ξ

Hall

Rapiejko

WO200058467-A1

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RESULT
AAY95032
Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of the invention.
            Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflammation; infection; fungal; bacterial; viral; HIV; allergy; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nerv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of their activities include immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers - \frac{1}{2}
                                                                                             Human clone
                                                                                                                                  19-JUN-2000
                                                                                                                                                                                                           AAY95032 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-2000; 2000WO-US07505
                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                    pffffaaiclvslvft 77
                                                                                                                                                                                                                                                                                                                                               AFWLTAAFCILSVLFT 94
                                                                                                                                                                                                                                                                                                                                                                                                                             LFTAGFAVGWGPIPWLLMSETFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMETLRPYG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis, hyperproliferative disorders e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-611712/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
                                                                                         vql_1 insertional variant ORF, SEQ ID NO:132
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396; 440pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0126502.
99US-0172410.
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                                                                                                                                                                                                             ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
3.6e-20;
hes 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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В

62 pffffaaiclvslvft 79 AFWLTAAFCILSVLFT 94 δÃ

19 LFTAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG

lfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvltksflpvvstfglqv 61

Query Match Best Local Similarity

43.3%;

Score 220; DB 21; Pred. No. 5.4e-20; 5; Mismatches 22;

Length 147; Indels

0

Gaps

0

39;

Conservative

15;

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24 - AUG - 1998;
24 - AUG - 1998;
09 - SEP - 1998;
28 - SEP - 1998;
25 - NOV - 1998;
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23-DEC-1998;
23-AUG-1999;
                                                                                     diagnostic primers and probes. Sequences AAY95024-Y95025, AAY95029 and AAY95031-Y95032 represent additional open reading frames (ORFs) that are encoded by deletional or insertional variants of the cDNA clones of the
                                                                                                                                                                                                                                                                                                insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                            lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. Sequences AAY95024-Y95025, AAY95029 and acceptance of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contracti
                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regime. Diseases or conditions that may be treated using the proteins nucleotides of the invention include autoimmune diseases; genetic % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and thrombolytic activity; anti-inflammatory activity; and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 351-352; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine activity; cell proliferation; differentiation; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-224657/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORF; variant
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147
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98US-0097659.
98US-0099618.
98US-0102092.
98US-0113645.
98US-0113646.
99US-0379246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US19351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rapiejko
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RESULT
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AAB66937
                                                                                                 В
                                                                                                                                                                                Query Match 42.7
Best Local Similarity 51.3
Matches 39; Conservative
                                                                                                                                                                                                                                                        The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66912-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is human GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders e.g. ischemia and diabetes - \,
  17-APR-2001
                       AAB66941;
                                           AAB66941 standard;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 81-82; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-2000;
13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GLUTX3
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27 - AUG - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
hypoglycaemia; glucose metabolism disorder; neurodegenerative di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000;
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                                                                                               AFWLTAAFCILSVLFT 94
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pflffaaiclvslvft 479
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DB; AAF55870.
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99US-0151140.
2000US-0184285.
2000US-0616132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-IB01042
(first entry)
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                                           Protein; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                             42.7%;
51.3%;
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Pred. No. 5.7e-19;
4; Mismatches 23;
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Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia, hypoglycaemia; glucose metabolism disorder; neurodegenerative of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr

disease.

Rattus sp

Rat

17-APR-2001 AAB66938;

(first entry)

AAB66938 standard; Protein;

503

464

pflffaaiclvslvft 479

11

79 AFWLTAAFCILSVLFT 94

404 lfimgyavgwgpitwllmsevlplrargvasglcvlaswltafvltksflpvvstfglqv 463

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Query Match
Best Local S
Matches 39
                                                                                                                                           The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence
                                                                                                                                                                                                                                                                                  Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                       Sequence
                                                                                                                                                                                                                                                           Claim 11; Page 83-84; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUTX3
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112615/12
                                                                                                                                                                                                                                                                                                                                                                     Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                (UYLA-) UNIV LAUSANNE.
                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2000; 2000WO-IB01042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypoglycaemia; glucose metabolism
                                                                                                                                  for GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001
Local Similarity 51.3 tos 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consensus sequence
                                                                                                         507 AA;
                                                                                                                                                                                                                                                                                                                                                                     Ibberson
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0143907.
99US-0151140.
2000US-0184285.
2000US-0616132.
                                                42.7%;
51.3%;
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                                                                                                                                                                                                                                                                                                                                                                     Uldry
                                     ; Score 217; DB 22;
; Pred. No. 5.7e-19;
14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                     X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder; neurodegenerative
                                                              Length 507;
                                       Indels
                                      0;
                                     Gaps
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AAM25722
ID AAM2
      Вb
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Best Local Similarity
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                       dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                   antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:1237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM25722 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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443 vltkyfllavnafglqvpffffsaiclislift 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paaafnyltlipllatm1fimgyamgwgpitw1lmsev1p1rargvasg1cv1vsw1taf 442
                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF55871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503
   disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0151140.
2000US-0184285.
2000US-0616132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ibberson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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45.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 214; DB 22;
Pred. No. 1.3e-18;
7; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,:
                                                                                                                                                                                                                                                                                                                        anaemia;
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18-OCT-2000

(first

entry)

termination sequence hybridisation assay;

Protein identification; signal transduction pathway; metabolic pathway;

genetic

mapping;

gene expression

control;

promoter;

Arabidopsis thaliana protein fragment SEQ ID NO: 45980

AAG37400

AAG37400 standard; Protein;

RESULT

В QΥ

12 LAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEF l lagrkvllfvsgyvvgwgpitwllmsevlplrargvasglcvlaswltafvltksf 56

Matches

Conservative

Mismatches

13;

Indels

Gaps

0

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Query Match
Best Local
                                                                                                                                                                                                        encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosts of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders,
                                                                                                                                                                                                                                                                                                                                                                             antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HTV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAH92166. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                          antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
                                                                          Sequence
                                                                                                                neurological disorders.
                                                                                                                                 rhinitis, asthma, diabetes,
Alzheimer's disease, Parkin:
                                                                                                                                                                     anaemia, platelet disorders, thrombocytopaenia, wounds, osteoporosis, severe combined immunodeficiency, eczema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorder.
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                            70
                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1217pp; English
37.2%;
57.1%;
                                                                                                                                   Parkinson's disease,
                                                                                                                                                 cancer, multiple sclerosis,
Score 189; DB 22;
Pred. No. 1.8e-16;
                                                                                                                                 neurodegenerative and
                 Length 70;
                                                                                                                                                       depression,
                                                                                                                                                                       allergic
                                                                                                                                                                                            burns, ulcers,
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18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 21-JUN-1999; 22-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 28-JUN-1999;	04-JUN-1999 07-JUN-1999 08-JUN-1999 10-JUN-1999 10-JUN-1999 14-JUN-1999 16-JUN-1999 17-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999	04 -MAY -1999 05 -MAY 1999 06 -MAY 1999 06 -MAY 1999 06 -MAY 1999 11 -MAY 1999 14 -MAY 1999 14 -MAY 1999 14 -MAY 1999 14 -MAY 1999 17 -MAY 1999 19 -MAY 1999 20 -MAY 1999 21 -MAY 1999 21 -MAY 1999 22 -MAY 1999 23 -MAY 1999 24 -MAY 1999 25 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999 27 -MAY 1999	25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 19-APR-1999 19-APR-1999 23-APR-1999 23-APR-1999 23-APR-1999 23-APR-1999	Arabidopsis EP1033405-A2 06-SEP-2000. 25-FEB-2000;
99US-0139461. 99US-0139462. 99US-0139463. 99US-0139750. 99US-0139763. 99US-013989. 99US-0140353. 99US-0140354. 99US-014065. 99US-0140823.	990S-0137502 990S-0137502 990S-0138724 990S-0138540 990S-0138847 990S-0139452 990S-0139453 990S-0139454 990S-0139456 990S-0139456 990S-0139456 990S-0139459 990S-0139459	99US 0132464 99US 0132485 99US 0132486 99US 01322863 99US 0134256 99US 0134218 99US 0134211 99US 0134211 99US 0134211 99US 0134211 99US 013421 99US 013421 99US 0134768 99US 0135124 99US 0135629 99US 0135629 99US 0136782 99US 0137522	99US-0123180 99US-0123180 99US-0123548 99US-0125788 99US-0126264 99US-0126785 99US-0126785 99US-0128714 99US-0128234 99US-0128234 99US-0128214 99US-0130077 99US-0130449 99US-0131449 99US-0131449 99US-0132407	thaliana.
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KW termin
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31;
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                                                                                                  Sequence 12, Application US/08928692 Patent No. 5958727
                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                  GENERAL INFORMATION:
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 APPLICANT:
APPLICANT:
TITLE OF IN
                                                  APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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APPLICATION NUMBER: 09/0:
FILING DATE: 26-FEB-1998
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    365 MSYVSIVAIFGEVAFFEVGPGPIPWFIVAELFSQGPRPAAIAVAGESNWTSNFIVGLLFQ 424
                                                                                                                                                                                                    425 YIAELLGPY-VFIVFAVLLLLFFIFT 449
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ZIP: 02110-2804
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     T: Hansen,
INVENTION:
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                                                                 Brody,
                                     Lamsa,
                                                   Yaver,
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                                    Michael
                                                  Howard
Deborah S.
                 Kim
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Methods for Modifying the Production
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                                                                                                                                                                                                                                                                                                         Sequence 13, Appr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                     TITLE OF INVENTION: Methods for MOTIFIE OF INVENTION: a Polypeptide
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CORRESPONDENCE ADDRESS: ADDRESS: No. 59587270 No. 5958727disk of No. 5958727th America,
CURRENT APPLICATION DATA:
                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   454 FQYIADFCGPY-VFFLFAGVLLAFTLFT
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                                                                                                                 CITY: New York
STATE: NY
                        COMPUTER: IBM COR
OPERATING SYSTEM:
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                                                        MEDIUM TYPE: Diskette
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ZIP: 10174
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TELEPHONE: 212-878-9655
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             SOFTWARE:
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             FastSEQ for Windows Version
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SYSTEM: DOS
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33.0%;
                                                                                                                                                                                                                      Methods for Modifying the Production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 130; DB 2;
Pred. No. 3.3e-08;
6; Mismatches 39;
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US/08/928,692

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                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods for modifying the Production TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 TFAFFAGLSCLSTIF 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 VFAAFYALGIGTVPW-QQSELFPQNVKGIGTSYATATNWAGSLVIASTFLTMLQNITPAG 511
                                                                                                                                                                                                                                                                            COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Lex
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG 78
STRANDEDNESS:
                                                                                                                                REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 12-SEF
                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
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               amino acid
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                              488 amino acids
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Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brody, Howard
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                                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                                                                                                                                                                                                                                 Dos
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                                                                                                                                                                                                                                 US/08/928,692
                                                                                                                                               33,728
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                                                                                                                                 4944.200-US
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                                                                                                                                                                                                                     ; MOLECULE TYPE: US-09-031-392-5
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                                                                                                                                   Matches
                                                                                                                                                 Best Local Similarity
                                                                                                                                                                 Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/031,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                357
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417 -----GLLFPSATFYLGAYVFIVFTVFLVIF 442
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                               64 TKEFNSIMEILRPYGAFWLTA----AFCILSVLF 93
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07:
LECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meiklejohn, Ph.D., REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 225 F
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                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
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                                                                                                4 DVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLV 63
                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/09/031,392
26-FEB-1998
                                                                                                                                                 24.2%; Score 123; DB 2; 29.8%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%; Score 124; DB 2; 32.2%; Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Windows95
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                                                                                                                                 Indels
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US-09-299-549-5
                                                                                                                                                                                         Sequence 4, Application US/09031392 Patent No. 5942398
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                   GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Weng, Xun
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/0
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: 09/031,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                       64 TKEFNSIMEILRPYGAFWLTA----AFCILSVLF 93
                      CITY:
                          ADDRESSEE: Fish & KICHWINGERSTREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meiklejohn, Ph.D., An REGISTRATION NUMBER: 35,283 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COLOPERATING SYSTEM:
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CITY: E
     STATE:
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                                                                                                                                                                                                                                                                                          -----GLLFPSATFYLGAYVFIVFTVFLVIF 442
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Boston
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29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 123; DB 4;
Pred. No. 2.3e-07;
1; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 494;
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Best Local Similarity
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APPLICANT: Tartag
APPLICANT: Weng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                    FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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                 07334/072002
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Pred. No. 2.9e-07;
5; Mismatches 36;
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Best Local Similarity
                                                                          Query Match
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TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLOTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/031,392 FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
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LENGTH: 534 amino acids
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                                          y match 24.0%; Score 122; DB 2; Local Similarity 31.8%; Pred. No. 2.3e-07; tes 27; Conservative 20: Vicari
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OPERATING SYSTEM:
                                                                                                                                                         TOPOLOGY: linear
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ZIP: 02110-2804
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                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
              9 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 68
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                                              34;
                                                                          Length 383,
                                            Indels
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                                                                                                         RESULT
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APPLICANT:
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; Sequence 3, Application US/09299549
; Patent No. 6136547
Sequence 6, Application US/09031392
Patent No. 5942398
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACT
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 35,283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: GLUTEX AND USES THEREOF
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                                                                                                                                                                                              315 YVEQLCGPY----VFIIFTVLLVLF 335
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                      24.0%;
  NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                                                                                                                                                                                                                  Score 122; DB 4;
Pred. No. 2.3e-07;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                    34; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length 383;
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                    1.
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TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS

ENCODING GLUTEX AND USES THEREOF

Fish & Richardson P.C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: US-09-031-392-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09299549 Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                           APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 YVAEAMGPY-VFLLFAVLLLGFFIFT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 MSYVSIVAIFGFVAFFEIGPGPIPWFIVAELFSQGPRPAAMAVAGFSNWTSNFIIGMGFQ 439
APPLICATION NUMBER: US/0 FILING DATE: 26-APR-1999 NIOR APPLICATION DATA:
                                                                  OPERATING SYSTEM:
SOFTWARE: FastSEQ
                                                                                                        COMPUTER:
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SIMEILRPYGAFWLTAAFCILSVLFT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                         Boston
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                                                                                                                                                                                                                        225 Franklin Street
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                                                                                                 IBM Compatible
                                                                                                                                                                                                                                          Fish & Richardson P.C
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                                                                                  Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%; Score 120.5; DB 2; 29.1%; Pred. No. 4.9e-07; tive 22; Mismatches 38;
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                                  US/09/299,549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.1
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                 SEQUENCE CHARACTERISTICS
                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2586
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fischbarg, Jorge APPLICANT: Czegledy, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                   COUNTRY: 00... 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                   STREET: New York
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STRANDEDNESS:
                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                 NAME: Tang, Henry Y.S
REGISTRATION NUMBER:
                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-DEC
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Brumbauyn, or use STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 SIMEILRPYGAFWLTAAFCILSVLFT
                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 68
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                 amino acid
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                             492 amino acids
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                                                                                  212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheung, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iserovich, Pavel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                             14-DEC-1994
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29.1%;
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                                                                                                                                                                                                                                US/08/355,844
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                                                                                                                                              29,705
                                                                                                                                                                                                                                                                                                                                                                                                                                 Graves, Donohue & Raymond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120.5; DB 4
Pred. No. 4.9e-07;
2; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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PCT-US95-16126-3
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Best Local Similarity
                                        INO:
ITYPE: amino acids
STRANDEDNESS: Sir
TOPOLOGY:
OLECULF
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Li, Jun
APPLICANT: Cheung, Min
TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
TITLE OF INVENTION: STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
FEATURE:
                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/355,844 FILING DATE: 14-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 YVEQLCGPY----VFIIFTVLLVLF 444
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                                                                                                                                                                                                                    NAME: Tang, Henry Y.S. REGISTRATION NUMBER: 29 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.492
OTHER INFORMATION:
OTHER INFORMATION:
                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFN 68 :::|: : | | | | | | | | | |
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Czegledy, Ferenc
Iserovich, Pavel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
1..492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%; Score 113; DB 2; 30.6%; Pred. No. 4.1e-06; tive 20; Mismatches 35
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                                                                                                                                                                                                                                29,705
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LOCATION: Peptide
LOCATION: 1..492
OTHER INFORMATION: F
OTHER INFORMATION: G
PCT-US95-16126-3
Search completed: February 13, 2002, 21:51:38 Job time: 6265 sec
                                                                                   Db
                                                                                                                  Qy
                                                                                                                                                     Дb
                                                                                                                                                                                  Qy
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                  424 YVEQLCGPY----VFIIFTVLLVLF 444
                                                                                                                                                     364 MSYLSIVAIFGFVAFFEVGPGPIPWFIVAELESQGPRPAAIAVAGFSNWTSNFIVGMCFQ 423
                                                                                                                  69 SIMEILRPYGAFWLTAAFCILSVLF 93
                                                                                                                                                                     26;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                       22.2%; Score 113; DB 5; Length 492; 30.6%; Pred. No. 4.1e-06; tive 20; Mismatches 35; Indels
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Title:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                        Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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508
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219241 seqs, 76174552 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                            SUMMARIES
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DG :- ] +		Ouerv				
No.		Match	Length	DB	ID	Description
	7 .	δ :	348	2	492	probable sugar tra
2	1.	33.8	487	Ν	678	tical prot
w	162.5	32.0	516	2		Ğ.
4	9.	31.4	514	2	500	Ð
ۍ	9.		523	Ν	S25015	t t
6	158.5	<del>-</del>	376	2	T43176	3
7	158	31.1	493	2	669	protein FlN21.12 [
œ	158	۲.	521	2	G84864	Œ
9	157.5	<u>,                                    </u>	522	2	S12042	glucose transport
10	1.57.5	<b>⊢</b>	522	Ν	E86246	
11	157	0	467	2	682	ው
12	155.5	0	490	N	T14545	e sugar
13	155.5	0	534	N	843	hexose transport p
14	155	0.	457	Ν	E70070	
15	154.5	0	483	2	D96589	hypothetical prote
16	154.5	30.4	523	N	T10122	hexose transport p
17	152.5	0.	534	N	S14144	
18	151.5	9.	433	2	G86812	se proton-s
19	151	9.	582	2	F71431	_
20	150.5	9	580	N	D86426	
21	150	9	734	Ν	H86340	
22	149.5	9	557	ν	T38125	osito
23	146.5	8	472	2	S47089	0
24	146	ω.	472	Ν	B26430	
25	146	8	472	2	E85936	l prot
26	146	8	508	2	T05156	cose
27	145	8	613	2	T27077	ical prot
28	142.5	28.1	461	2	G85059	e suqa
29	4	28.1	729	2	T06127	sugar

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T27072
r10150
142
A31556
539
951
T43400
T01853
145
D84772
920
в86096
130
F65079
T10124

## ALIGNMENTS

RESULT 2  E96782 hypothetical protein F22H5.6 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: E96782 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 40B, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	Oy 6 HLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 65	C;Genetics: A;Gene: At2948020 A;Gene: At2948020 A;Map position: 2  Query Match Best Local Similarity 43.2%; Pred. No. 3.8e-12; Matches 38; Conservative 18; Mismatches 31; Indels 1; Gaps 1;	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84922 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-348 <sto> A;Cross-references: GB:AE002093; NID:g4249409; PIDN:AAD13706.1; GSPDB:GN00139</sto>	RESULT 1  D84922  probable sugar transporter [imported] - Arabidopsis thaliana  probable sugar transporter [imported] - Arabidopsis thaliana  probable sugar transporter [imported] - Arabidopsis thaliana  (c;Species: Arabidopsis thaliana (mouse-ear cress)  C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001  C;Accession: D84922  C;Accession: D84922  R;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y  M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  Nature 402 - 761-768, 1999

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monosaccharide transport protein STP4 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C; Accession: S25009
R; Sauer, N; Illig, J; Baier, K; Stadler, R.
submitted to the EMBL Data Library, June 1992
A; Description: A sink specific monosaccharid transporter from Arabidopsis th A; Reference number: S25009
A; Accession: S25009
A; Accession: S25009
A; Molecule type: mRNA
A; Residues: 1-514 <SAU>
A; Cross-references: EMBL:X66857; NID:g16523; PIDN:CAA47325.1; PID:g16524
C; Genetics:
A; Gene: STP4
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C;Superfamily: glucose transport protein
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R;Weber, H.; Borisjuk, L.; Heim, U.;
Plant Cell 9, 895-908, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monosaccharid transport protein - fava bean
C:Species: Vicia faba (fava bean)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change
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T12199
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A; Residues: 1-516 <WEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: A role for sugar transporters during seed development: molecular characterizat A; Reference number: 217451; MUID: 97355984
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A; Map position: 1
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-487 <STO>
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Best Local Similarity
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Pred. No. 2.2e-09;
Pred. No. 38;
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Pred. No. 2.4e-10;
21; Mismatches 35;
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A;Experimental source: strain PR745
C;Superfamily: maltose transport protein MAL61
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                   probable myo-inositol transport protein - fission yeast (Schizosaccharomyces C:Species: Schizosaccharomyces pombe C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-376 < YOS>
                                                                                                                                                                                                                                          R:YOShioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in Schizosaccharomyces pombe A;Reference number: 217323; MUID:98162722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: mRNA
A:Residues: 1-523 <SAUV
A:Residues: 1-523 <SAUS
A:Cross references: EMBL:X66856; NID:g19884; PIDN:CAA47324.1; PID:g19885
C:Superfamily: glucose transport protein
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submitted to the EMBL Data Library, June 1992
A;Description: Asince
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
                                                                                                                                                A; Cross-references: EMBL: D89252; NID: g1749711; PIDN: BAA13913.1;
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                                                                                                                                                                                                                                                                                                                     C; Accession:
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C;Keywords: sugar transport; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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Best Local
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Best Local :
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     30;
                   Similarity
                                                                                                                                                                                                                                                                                                                     T43176
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   Conservative
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                     31.2%;
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   22;
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Pred. No. 4.4e-09;
""" matches 31;
 Pred. No. 4.1
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 159.5; DB 2
Pred. No. 4.5e-09;
                     Score 158.5;
Pred. No. 4.
                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.50
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transporter
                     .le-09;
                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                    2;
 Indels
                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                      376;
                                                                                                                                                PID:g1749712
 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
Gaps
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2
                                                                                                                                                                                                                                                                                                                                                                         pombe) (
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QΥ

PAD----VHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW

57

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487 A;Accession: G84864
                                                                                                                                                                                                                                                                                                        R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                 probable membrane transporter [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Araba; Reference number: A86141; MUID:21016719

A;Accession: F96696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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                                                                  A; Map position:
C; Superfamily:
                                                                                                              A; Gene: At2g43330
                                                                                                                                  C; Genetics
                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-521 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-493 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein F1N21.12 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F96696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                       A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: G84864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005173; NID:g9828628; PIDN:AAG00251.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Theologis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 LELRLLEKLGPRLLYSMFSTFCLMAVMF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 HFSALCLSVGGTLVFVLTFALGAGPVPGLLLPEIFPSRIRAKAMAFCMSVHWVINFFVGL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 VGNLIISASFLTMMESITPTGTFALFAGFCFVGLV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 EFNSIMEILRPYGAFWLTAAFCILSVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
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                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLGLAWLAVGSMCLFTAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMAFLVTKEFNSIMEILRPYGAFWLTAAFCILSVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.;
                                                                  glucose
                                                                                                                                                       GB:AE002093;
                                                                    transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%;
      31.1%;
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                                                                                                                                                     NID: g2289003;
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  Score 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
    DВ
                                                                                                                                                       PIDN: AAB64332.1;
    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Davis, R.W.
The plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
      521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaul, S.; White, O.; Alonso
                                                                                                                                                         GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.; Khaykin, E.; .S.; Maiti, R.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                   Fujii, C.Y.;
L.; Tallon, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Map position: 1
C; Superfamily: glucose transport protein
                                                                                 A:Molecule type: DNA
A;Residues: 1-522 <STO>
A;Cross-references: GB:AE005172; NID:g5734730; PIDN:AAD49995.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                       Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucose transporter [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucose transport protein STP1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: glucose transport protein
C; Keywords: sugar transport; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Sauer, N.: Friedlaender, K.; Graeml-Wicke, U. EMBO J. 9, 3045-3050, 1990
                                                          C; Genetics:
                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                   A:Reference number: A86141; MUID:21016719 A;Accession: E86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: E86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: STP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X55350; A;Note: the sequence from Fig. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-522 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S12042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S12042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Primary structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S12042; S14627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 IIAQIFLTMLCHLK-FGLFLVFAFFVVVMSIF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 AEAAGTGMTFLILAGIAVLAVIF 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 PGELPKWYAIVVVTFICIYVAGFAWSWGPLGWLVPSEIFPLEIRSAAQSITVSVNMIFTF 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 WLAVLGLALYIVFFAPGMGPVPWTVNSEIYPQQYRGICGGMSATVNWISNLIVAQTFLTI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LVTKEFNSIMEILRPYGAFWLTAAFCILSVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 WLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 MEILRPYGAFWLTAAFCILSVLF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.0%;
33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic organization and heterologous expression of a \ensuremath{\mathsf{MUID}}\xspace:91005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g16519; PIDN:CAA39037.1; PID:g16520 is inconsistent with that from Fig. 1 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 157.5; DB 2
Pred No. 7.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.4e-09; 5; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.J.; Federspiel, N.A.; Kaul, Conway, A.B.; Conway, A.R.; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Creasy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - Sep - 1999
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                                                                                                                                                                                                                                                                                                                                                                                                Kim,
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probable sugar transporter protein - beet C.Species: Beta vulgaris (beet) C.Species: Beta vulgaris (beet) C.Pate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C.Accession: T14545 R.Chiou, T.J.; Bush, D.R. Plant Physiol. 110, 511-520, 1996 Plant Physiol. 110, 511-520, 1996 A.Title: Molecular cloning, immunochemical localization to the vacuole, and A.Reference number: Z18131; MUID:96351183 A.PACCESSION: T14545
                             A:Experimental source: tonoplast C:Superfamily: glucose transport protein
                                                                            A;Cross-references: EMBL:U43629; NID:g1209755; PIDN:AAB53155.1; PID:g1209756
C; Keywords: transmembrane
                                                                                                                                     A; Residues: 1-490 <CHI>
                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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A:Map position: 1
C:Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. D.; Sakano, H. D.; Sakano, H. D.; Southwick, A.M.; Sun, H.; Tallon, A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005173; NID:g6453876; PIDN:AAF09060.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-467 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A86141; MUID:21016719
A;Accession: B96829
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Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable sugar transporter, 77409-81599 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QУ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 IIAOIFLTMLCHLK-FGLFLVFAFFVVVMSIF 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LRMLEQLGSVLLNAIFGFFCVVAVIF 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTLFLSVGGMLLFVLSFATGAGPVPSLLLSEICPGRLRATALAVCLAVHWVINFFVGLLF 416
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33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 157; DB 2;
Pred. No. 7.3e-09;
7; Mismatches 32;
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                                                               R;Kunst, F.; Ogasawara, N.; Moszer, T.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bero, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Accession: E70070
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A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029;

PIDN:CAB15600.1; PID:g26361

not

A; Status: preliminary; nucleic acid sequence not shown; translation

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

metabolite transport protein homolog ywtG - Bacillus subtilis C;Species: Bacillus subtilis

C; Accession: E70070

A; Molecule

type: DNA : 1-457 <KUN>

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E70070
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                                                                                                                                                                                                                                                              C;Superfamily: glucose transport protein
C;Keywords: sugar transport; transmembrane protein
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C:Species: Chlorella kessleri
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X75440; NID: g408808; PIDN: CAA53192.1; PID: g408809
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-534 <STA>
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A; Accession: S38435
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S38435
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Best Local :
                                                            442 VIGQAFVSMLCAMK-FGVFLFFAGWLVIMVL
                                                                                                                            386 PHPVSAGV-
                                                                                        62 LVTKEFNSIMEILRPYGAFWLTAAFCILSVL
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 LSWNSGGTFSIYMVVCAFTVAF 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .12 LAVGSMCLEIAGFAVGWGDIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEENSIM 71
                                                                                                                                              2 PADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAF 61
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39.0%;
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                                                                                                                                                                                Score 155.5; DB 2;
Pred. No. 1.2e-08;
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Pred. No. 1.1e-08;
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                                                                                          92
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hypothetical protein T22H22.15 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Accession: D96589  
C.Accession: D96589  
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L. A.B.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alauther; J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; preliminary A.; Status; 
Search completed: February 13, 2002, 21:53:11 Job time: 6133 sec
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D96589
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C:GeneriywtG
A:Gene: ywtG
C:Superfamily: glucose transport protein
                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005173; NID:g3776581; PIDN:AAC64898.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-483 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.4%; Score 154.5; DB 2; Best Local Similarity 33.3%; Pred. No. 1.4e-08; Matches 31; Conservative 24; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.5%; Score 137, 20.2%; Best Local Similarity 35.7%; Pred. No. 1.2e-08; Matches 30; Conservative 19; Mismatches 35;
                                                                                                                                                                                                                        427 WIISETENELMN-WNPAGTEYVFATVCGATVIF 458
                                                                                                                                                                                                                                                                                                                                                                                                   367 ESAGVSSKIGMIAMVVVQVYTGSFSLGMGGIPWVIMSEIFPIDIKGSAGSLVTVVSWVGS 426
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                                                                                                                                                                                                                                                                                                       61 FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLF 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 IMEILRPYGAFWLTAAFCILSVLF 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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ovis aries sus scrofa bacillus su

P20303 P54723

homo sapien mus musculu homo sapien rattus norv saccharomyc saccharomyc saccharomyc

bos taurus

gallus gall

P27674 P11166 P17809 P14672 P46896 P19357 P42833 P39003

HXTD_YEAST HXT6_YEAST

HXT7_YEAST

GTR1_MOUSE GTR4_HUMAN

390 4451 4492 4492 509 4490 570 570

122 122 122 122 122 120.5 118.5 118.5 118

334 337 337 44 44 54 54

GTR1_CHICK

GTR4_RAT

YFIG_BACSU GTR1_BOVIN GTR1_HUMAN

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041144 ricinus com
P15686 chlorella k
P4558 klebsiella k
P4598 lescherichia
P09830 escherichia
P07423 ricinus com
P37021 escherichia
P09098 escherichia
P03098 escherichia
P03098 escherichia
P03098 chizosacch
P14246 mus musculu
Q39524 chlorella k
P12336 rattus norv
Q01440 leishmania
Q53731 acctobacill
Q57331 acctobacill
Q10710 ricinus com
P11169 homo sapien
P11169 homo sapien
P11169 homo sapien
P11169 homo sapien
P10870 saccharomyc
                                                                    (without alignments)
49.604 Million cell updates/sec
                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          ; Search time 69.48 Seconds
                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                       .....RPYGAFWLTAAFCILSVLFT
         Compugen Ltd
                                                                                                                                                                                         hits satisfying chosen parameters:
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                      100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                          February 13, 2002, 22:06:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSBC_BACSU
ITR1_SCHPO
GTR2_MOUSE
HUP2_CHLKE
GTR2_RAT
GTR1_LEIDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XYLT_LACBR
STA_RICCO
GTR3_HUMAN
GTR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                       HUP3_CHLKE
STC_RICCO
HUP1_CHLKE
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ARAE_KLEOX
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Listing first 45 summaries
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GALP_ECOLI
                                         sw model
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                                                                                                                    1 EPADVHLGLAWLAVGSMCLF...
                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                      OM protein - protein search, using
                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                 US-09-516-493-12
                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
Maximum Match 10
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Match Length DB
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155.5
154.5
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137.5
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137.5
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137.5
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133.5
130.2
130.2
120.5
127.5
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127.5
126.5
126.5
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Maximum DB
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                                                                                                                                                                                                   Embryophyta; Tracheophyta;
dons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                            STRAIN=CV. LANDSBERG ERECTA;
MEDLINE=9100595; PubMed=220537;
Sauer N., Friedlaender K., Graeml-Wicke U.;
"Primary structure, genomic organization and heterologous expression of a glucose transporter from Arabidopsis thaliana.";
EMBO J. 9:3045-3050(1990).
-i. FUNCTION: ACTIVE UPTAKE OF HEXOSES. PROBABLE GLUCOSE/HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                      SYMPORT.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugar transport; Symport.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GLUCOSE TRANSPORTER (SUGAR CARRIER).
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR: S12042; S12042.
InterPro; IPR003663; Sugar_trnsportr.
Interpro; IPR003663; Sugar_trnsportr.
Interpro; IPR003662; sub_trnsportr.
IPR00103; Sugar_tr; 1.
PR1NTS; PR00171; SUGRTRNSPORT.
PRNTS; PR00171; SUGRTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1: 1.
PROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
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POTENTIAL.
POTENTIAL.
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                                                                          PRT;
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                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
133
161
161
188
220
220
305
341
369
405
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                          STP1_ARATH
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TRANSMEM
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                                                                                       P23586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                        STP1_ARATH
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rattus norv saccharomyc zymomonas m saccharomyc oryctolagus

SNF3_YEAST ITR1_YEAST

CANFA ITR2_YEAST

GTR3_

GTR3_RAT

canis famil

mnscnln

mus

P32037 m Q12300 s Q92253 n P30606 : P21906 ; Q07647 P47842

GTR3_MOUSE RGT2_YEAST

ZYMMO

RABIT

SHEEP GTR2_CHICK

RCO3_NEUCR

rattus norv neurospora

ovis aries

qallus

3;

Gaps 61

5;

Length 534; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis (Castor bean).
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Malpighiales, Euphorbiaceae, Ricinus.
                                                                                                                                                                                                                                2 PADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLÜLAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. CARMENCITA; TISSUE=Cotyledon; Weig A., Franz J., Sauer N., Komor E.; "Isolation of a family of cDNA-clones from Ricinus communis L. with close homology to the hexose carriers."; J. Plant Physiol. 143:178-183(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 154.5; DB 1; Length 523; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       074804EFA3A27F6B CRC64;
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                                                                DB 1;
                                                             30.6%; Score 155.5; DB 38.5%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GICCO
STGNUARL,
041144; 041147;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                           Pred. No. 1.5e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 442 VIGQAFVSMLCAMK-FGVFLFFFAGWLVIMVL 471
                                                                                                                                                                                                                                                                                                                            LVTKEFNSIMEILRPYGAFWLTAAFCILSVL 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella.
NCBL_TaxID=3074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
52E03715F3726017 CRC64;
                                                                CYTOPLASMIC (POTENTIAL).
68A6C72AFFD90380 CRC64;
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-!- FUNCTION: ACTIVE UPTAKE OF HEXOSES.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                          Query Match 31.0%; Score 157.5; DB 1
Best Local Similarity 33.7%; Pred. No. 9.7e-08;
Matches 31; Conservative 23; Mismatches 37
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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PRINTS; PR00171; SUGRTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                      Pfam; PF00083; sugar_tr; 1. PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolf K., Tanner W., Sauer N.;
"The Chlorella H+/hexose cotransporter gene.";
Curr. Genet. 19:215-219(1991).
-!- FUNCTION: ACTIVE UPTAKE OF HEXOSES.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorella kessleri
                                                                                                                                                                                                            Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                   EMBL; X55349; CAA39036.1; -. PIR; S07096; S07096.
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"The hexose carrier from Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3074;
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ansport; Sugar transport;
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15-JUL-1998 (Rel. 1
30-MAY-2000 (Rel. 1
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PRINTS; PR00171; SUGERTRNSPORT.
PRINTS; PR00172; GLICTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSP
                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                             STRAIN-PR745;
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InterPro; IPR003662; sub_trnsportr.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                  FUNCTION: TRANSPORTER FOR MYO-INOSITOL. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
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                                                                                                                 X99105; -; NOT_ANNOTATED_CDS.
Z95334; CAB08597.1; -.
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SUGAR_TRANSPORT_2;
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Shatwell K.P., Charalambous B.M., McDonald T.P.,
"Cloning, sequencing, and expression of the araE
oxytoca 8017, which encodes arabinose-H+ symport
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                   InterPro; IPR003663;
InterPro; IPR003662;
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-!- FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=8017
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                        European Bioinformatics Institute.
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SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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                                                                                           non-profit institutions as long
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s requires a license agreement (See
an email to license@isb-sib.ch).
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IPR003662; sub_trnsportr.
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DRTER (ARABINOSE TRANS
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STRAIN=K12 / MG1655;
STRAIN=812 / MG1657;
PubMed=9278503;
                                                                                                                                                                                                                                                        MEDLINE=88228015; PubMed=2836407; Maiden M.C.J., Jones-Morthmer M.C., Henderson P.J.F.; Maiden M.C.J., Sequence, and overexpression of the coding for arabinose-proton symport in Escherichia col J. Biol. Chem. 263:8003-8010(1988).
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar transport; Transmembrane;
TRANSMEM 23 43 POTENTIAL.
    SEQUENCE FROM
                                            Science
                                                                                     Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
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MEDLINE=87115869; PubMed=3543693;
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                                         complete genome sequence nce 277:1453-1474(1997).
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03732; AAA23469.1;
EMBL; X00272; CAA25075.1;
EMBL; U29581; AAB40488.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-:- FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE WITH
-THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The araE low affinity L-arabinose sequence, transcription start site regulatory proteins.";
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InterPro; IPR003662; sub_trnsportr.
Pfam; PF0088; sugar_tr 1
PRINTS; PR00171; SUGRTRNSPORT.
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MEDLINE=21074935; PubMec
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AE005513; AAG57953.1;
AP002563; BAB37121.1;
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SUGAR_TRANSPORT_2; 1.
transport; Transmembrane;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
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01-OCT-1996
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InterPro; IPR003662; sub_trnsportr.
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PS00217; SUGAR_TRANSPORT_2; 1
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RESULT 9
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InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97426617; PubMed=9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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20-AUG-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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J. Biol. Chem. 262:13928-13932(1987).
                                                                                                                                                                  Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLING=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plun
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER).
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mammalian and bacterial sugar Nature 325:641-643(1987).
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Henderson P.J.F
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                                                                                                                                                   R.A., Blattner F.R.;
                                                                                                  409:529-533(2001).
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395
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Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
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Nucleic Acids Res. 16:4097-4109(1988).
-!- FUNCTION: UPTAKE OF D-XYLOSE ACROSS THE BOUNDARY MEMBRANE
THE CONCONITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEM
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EcoGene; EG11076; xylE
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InterPro; IPR003662; sub_trnsportr.
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rancoz end of the malEFG operon in E.coli: localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88234001; PubMed=2836810;
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MISCELLANEOUS: E.COLI HAS TWO D-XYLOSE TRANSPORT SYSTEMS THAT ACCUMULATE SUGAR AGAINST A CONCENTRATION GRADIENT: THE XYLE SYSTEM WHICH UTILIZES THE ELECTROCHEMICAL GRADIENT OF PROTONS AND THAT IS INSENSITIVE TO COLD OSMOTIC SHOCK AND THE XYLF SYSTEM THAT USES A HIGH-ENERGY PHOSPHATE COMPOUND AND IS SENSITIVE TO COLD OSMOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A26430; A26430.
A27418; A27418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X06663; CAA29863.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U00006; AAC43125.1; -. AE000476; AAC77001.1; -. AE005636; AAG59230.1; -. AP002568; BAB38437.1; -.
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                      Similarity
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POTENTIAL.
                    Score 140.5; DB : Pred. No. 3.5e-06
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T., Tanaka M., Tobe T.,
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P46333; 0322
01-NOV-1995
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                                                                              PRINTS; F
PROSITE;
                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          general stress transcription factor sigmaB.";
Microbiology 145:1069-1078(1999).
-!- FUNCTION: COULD SERVE EITHER A NUTRITIONAL
                                                                                                      InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00003; sugar_tr; 1.
                                                                                                                                                        EMBL; AB005554; BAA21604.1; EMBL; Z99124; CAB16017.1;
                                                                                                                                                                                                                                                between the Swiss Institute of Bioinfi
the European Bioinformatics Institute.
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              TRANSMEM
                           TRANSMEM
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                                                     Pransport;
                                                              PROSITE; PS00216; SUGAR_TRANSPORT_1; PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                             SubtiList; BG11360; csbC
                                                                                                                                                                                                                                                                                                                                                                                  Akbar S., Lee S.Y., Boylan S.A., Price C.W.; "Two genes from Bacillus subtilis under the
                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE=99303315; PubMed=10376822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Submitted (NOV-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
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NCBI_TaxID=1423;
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Last
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Best Local Similarity
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      PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
Transmembrane; Sugar_transport; Glycoprotein.
                                               InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; Pf00083; sugar_tr : 1
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                   EMBL; Z99532;
                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                              Niederberger C., Graub R., Schweingruber A.-M., Fankhauser H., Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.; "Exogenous inositol and genes responsible for inositol transport are required for mating and sporulation in Shizosaccharomyces pombe."; Curr. Genet. 33:255-261(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHPO
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CONFLICT
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                                                                                                                                                                                                                                                                                                          STRAIN=972;
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                                                                                                                                                                                                                                        tles S., Churcher C.M., Wood V., Barrell B.G., Rajand mitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION. TRANSPORTER FOR MYO-INOSITOL. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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(Rel. 40, Last annotation update)
L TRANSPORTER 1.
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                                                                                                                                                                commercial
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RESULT 13
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                     TISSUE SPECIFICITY STRAIN=C57BL/6;
MEDLINE=93170163; Pu
Smith D.E., Gridley
                                                                                                                               SEQUENCE OF 384.496 FROM N.A.
MEDLINE=92111400; PubMed=1765007;
Hogan A., Heyner S., Charron M.J., C
Jenkins N.A., Thorens B., Schultz G.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Liver;
                                                                                             "Glucose transporter gene expression Development 113:363-372(1991).
                                                                                                                                                                                                                                                    transporter protein
                                                                                                                                                                                                                                                                    MEDLINE-89366666; PubMed=2771649;
Asano T., Shibasaki Y., Lin J.L., Akanu
"The nucleotide sequence of cDNA for a
                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                           Suzue K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Liver;
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCOSE TRANSPORTER TYPE 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTR2_MOUSE
                                                                                                                                                                                                                                    Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90098776; PubMed=2602116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P14246;
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                                                                                                                                                                                                                                    Acids
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                                                                                                                                                                                                                                                                                                                                                                                   Lodish H.F., Thorens B.; of the mouse liver glucose transporter."; cids Res. 17:10099-10099(1989).
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(Rel. 33, I)
(Rel. 35, I)
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                   PubMed=1289053,
                                                                                                                                                                                                                                17:6386-6386(1989).
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33.3%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (F

N-LINKED (GLCNAC. . .) (F

N-LINKED (GLCNAC. . .) (F

N-LINKED (GLCNAC. . .) (F

N-LINKED (GLCNAC. . .) (F
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3B7C5EFF86C596AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                          Akanuma Y.,
                                                                                                                                                     Copeland N.G., Gilbert D.J.,
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                                                                                                                                                                                                                                                                      mouse liver-type
                                                                                                               early mouse embryos.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                        Takaku F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                          Oka Y.;
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Matches
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Best Local
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CONFLICT
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PRINTS; PR00171; SUGETRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X16986; CAA34855.1; -. EMBL; X15684; CAA33719.1; -. EMBL; S77926; AAB20847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Sugar transport; Transport; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  postimplantation mouse embryos.";
Development 116:555-561(1992).
                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                   DOMAIN
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1095438; Slc2a2.
InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
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                                                                                                                                                                                                                                                                                                    RANSMEM
393 AWMSYVSMTAIFLFVSFFEIGPGPIPWFMVAEFFSQGPRPTALALAAFSNWVCNFVIALC
                                10 AWLAVGSMC---LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASSAA MEMBRANE OF HEPATCOYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; IT MAY COMPRISE PART OF THE GLUCOSE-SENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUCOSE IN THE SMALL INTESTINE & KIDNEY. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
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                                                                        1 Similarity 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00172; GLUCTRNSPORT. PR01191; GLUCTRSPORT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ential screening of a PCR-generated mouse embryo cDNA library: transporters are differentially expressed in early
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                                                                      Conservative
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                                                                                       27.0%;
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                                                                                                                                                            MW;
                                                                      17;
                                                                                                                                                      CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (PO'
G -> D (IN REF. 2).
N -> T (IN REF. 2).
S -> T (IN REF. 2).
L -> F (IN REF. 2).
P -> S (IN REF. 1).
P -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                    Score 137; DB 1;
Pred. No. 7.7e-06;
7; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          symporter.";
Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998
15-JUL-1998
15-JUL-1998
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                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; sub_trnsportr.
Pfam; PF00083; sugar_tr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95175627; PubMed=7870840;
Stadler R., Wolf K., Hilgarth C., Tanner W.
"Subcellular localization of the inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H(+)/HEXOSE
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00216; PROSITE; PS00217;
                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                            Multigene
                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00172; GLUCTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X66855; CAA47323.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella.
                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nt Physiol. 107:33-41(1995).
FUNCTION: ACTIVE UPTAKE OF GALACTOSE
                      YGAFWLTAAFCTLSVLF
                                            ICVYVAAFAWSWGPLGWLVPSEIQTLETRGAGMSMAVIVNFLFSFVIGQAFLSMMCAMR- 457
                                                                   MCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRP 76
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                        Transport;
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                                                                                                                                                                                                                                                                                                                                     SUGAR_TRANSPORT_1; 1
SUGAR_TRANSPORT_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36, Last sequence update)
36, Last annotation update)
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32.5%;
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                                                                                             Mismatches
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(See http://www.isb-sib.ch/announce/
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                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                        Symport; Repeat;
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                                                                                             Indels
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            SEQUENCE
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PRINTS; PR00171; SUGRTRUSPORT.
PRINTS; PR00172; GLUCTRUSPORT.
PRINTS; PR01191; GLUCTRSPORT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the swiss institute. There are no recurrence the European Bioinformatics Institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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Thorens B., Sarkar H.K., Kaback H.R., Lodish H.F.;
"Cloning and functional expression in bacteria of a novel glucose transporter present in liver, intestine, kidney, and beta-pancreatic islet cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GLUCOSE TRANSPORTER TYPE 2, LIVER.
SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTR2_RAT
P12336;
                                     CARBOHYD
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InterPro; IPR003663; Sugar_trnsportr.
InterPro; IPR003662; Sub_trnsportr.
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                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00216; SUGAR_TRANSPORT_1; 1. PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE BETA CELLS; IT MAY COMPRISE PART OF THE GLUCOSE SENSING MECHANISM OF THE BETA CELL. IT MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE & KIDNEY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: PRESENT IN LIVER, INTESTINE, KIDNEY AND BETA-PANGREATIC ISLET CELLS.

SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTER FAMILY.

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HEPATOCYTES & IS RESPONSIBLE FOR UPTAKE OF GLUCOSE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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       57085 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          transport;
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (GLCNAC. . .) (POTENTIAL)
W: 075AB81E55CF33F7 CRC64;
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                                                                                                            Matches
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Best Local :
443 VCNFIIALCFQYIADFLGPY-VFFLFAGVVLVFTLFT 478
                                                      383 LGLVLLDKFTWMSYVSMTAIFLFVSFFEIGPGPIPWFMVAEFFSQGPRPTALALAAFSNW 442
                         58 FMAFLVTKEFNSIMETLRPYGAFWLTAAFCILSVLFT
                                                                  7 LGL-----AWLAVGSMC---LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNW
                                                                                                            32;
                                                                                                                       Similarity
                                                                                                          Conservative
                                                                                                                       26.6%;
                                                                                                         17;
                                                                                                                      Score 135; DB 1;
Pred. No. 1.2e-05;
                                                                                                          Mismatches
                         94
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                                                                                                                                 Length 522;
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seq length:
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                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
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508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
            sp_rodent:*
sp_virus:*
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100.509 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
- :	508	100.0	478	11	Q9JJZ1	Q9jjzl rattus norv
2	508	100.0	479	11	Q9JMA6	rattus
ω	482	94.9	477	11	Q9JJZ0	Q9jjz0 mus musculu
4	477	93.9	477	11	Q9JJP4	Rum
(J	477	93.9	477	11	Q9J1F3	if3 mus
6	457	90.0	477	4	Q9NSC4	c4 homo
7	454	89.4	477	4	Q9NY64	homo
8	222	43.7	433	υı	Q9V610	dros
9	220	43.3	507	4	Q9UGQ3	Q9ugq3 homo sapien
10	220	43.3	539	ų	Q9VU17	
11	219	43.1	489	Ŋ	Q9V609	
12	200.5	39.5	463	10	Q9MAA4	Q9maa4 arabidopsis
13	189.5	37.3	465	5	Q9V848	Q9v848 drosophila
14	187.5	36.9	348	10	Q9ZU87	Q9zu87 arabidopsis
15	186	36.6	444	ر.	Q9V3G0	Q9v3q0 drosophila
16	176.5	34.7	133	10	Q9LEG2	Q9leg2 lycopersico
17	171.5	33.8	487	10	Q9FRL3	Q9frl3 arabidopsis
18	169.5	33.4	621	6	Q9BE72	Q9be72 macaca fasc
19	168.5	ני	510	10	065322	OSSROO Detunia hyb

Q9LKH1
040373
09LM67
09SYQ3
Q9C757
023492
9CFH3
Q9ZS76
Q9STA9
Q9FIF2
Q9ZVM0
P96742
RT5
Q39416
Q9SCW6
826W6Ö
Q9CA87
Q9SXB1
022848
Q9FYG3
Q06312
Q39228
Q9VNJ2
Q9LN48
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## ALIGNMENTS

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"GLUTX1: A novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";

J. Biol. Chem. 275:4607-4612(2000).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SUBLIARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL; AJ245935; CAB75729.1;

InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; sugar_transporter.
Pfam; PP00083; sugar_transporter.

PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09JJZ1 PRELIMINARY; PRT; 478 AA.
09JJZ11,
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                             Transmembrane.
SEQUENCE 478 AA; 51458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=20138191; PubMed=10671487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUTX1.
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                                  363 EPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMA 422
 61 FLYTKEFNSIMEILRPYGAFWLTAAFCILSVLFT 94
                                                                                                                           Local Similarity
                                                                        1 EPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMA 60
                                                                                                          100.0%; Score 508; DB 11; ilarity 100.0%; Pred. No. 6.4e-42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                   95841FC1F18C9EE9 CRC64;
                                                                                                                                            Length 478;
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RESULT
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Best Local S
                                         Ibberson M.R., Uldry M.A., Thorens B.;
"GLUTX1: A novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";
J. Biol. Chem. 275:4607-4612(2000).
-i. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-i. SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AJ245936; CAB75719.1; -.
                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
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01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-JUN-2001 (TrEMBLrel. 17,
GLUCOSE TRANSPORTER 8.
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Mammalia; Eutheria; Rodentia;
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InterPro; IPR003663; Sugar transporter.
Pfam; PF00083; sugar_tr 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of a new putative glucose transporter.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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                         MGI:1860103;
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IPR003662; sub_transporter
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                         Glutx1.
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01-OCT-2000 (TrembLrel.
01-JUN-2001 (TrembLrel.
01-JUN-2001 (TrembLrel.
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Pfam; PF00083; Sugar_tr; 1.

PRINTS; PR00171; SUGRTRNSPORT.

PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PRINTS; PR00171; SUGRTRNSPORT
PROSITE; PS00216; SUGAR_TRANSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y17802; CAB89815.1; MGD; MGI:1860103; GlutX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:16275-16280(2000).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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InterPro; IPR003663; Sugar_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doege H., Schuermann A., Bahrenberg C., Brauers A., Joost "GLUT8: A novel member of the sugar transport facilitator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20283667; PubMed=10821868;
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PRELIMINARY;
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Pred. No. 6.7e-39;
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Pred. No. 2.2e-39;
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Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000)
-i-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROT
-i-SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL. AF233061; AAF78366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20319023; PubMed=10860996;
Carayannopoulos M.O., Chi M.M.Y., Cui Y., Pi
McKnight R.A., Mueckler M., Devaskar S.U., M
"GLUT8 is a glucose transporter responsible
                                                                              glucose transport activity.";
J. Biol. Chem. 275:16275-16280(2000)
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01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
GLUCOSE TRANSPORTER 8.
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Mammalia; Eutheria; Primates; Catarrhini;
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SEQUENCE 477
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PRINTS; PR00171; SUGRTRNSPORT
InterPro; IPR003662; sub_transporter
InterPro; IPR003663; Sugar_transporter
Pfam; PF00083; sugar_tr; 1
                                                                                                        Doege H., Schuermann A., Bahrenberg C., Braue "GLUT8: A novel member of the sugar transport
                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=TESTIS;
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                                      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; Y17801; CAB89809.1; -.
                                                                                                                                   MEDLINE=20283667, PubMed=10821868;
                                                                                                                                                                                        NCBI_TaxID=9606;
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InterPro; IPR003663; Sugar_transporter.
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Pred. No. 6.7e-39;
6; Mismatches 3
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Sciurognathi; Muridae;
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nsport facilitator
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GLUCOSE TRANSPORTER.
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SEQUENCE 477
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                                             Q9V610
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"GLUTX1: A novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues.";
J. Biol. Chem. 275:4607-4612(2000).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                             InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr 1.
PRINTS; PR00171; SUGRTTRNSPORT.
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EMBL; AJ245937; CAB75702.1; -.
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Pred. No. 1.2e-36;
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Dovielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris M., Gang F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M.,
RA Rainert K., Remington K., Saunders R., D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wann Z.-Y. Wassarman D. A. Weinster E., Wang A.H., Wang X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSFORT.
PRINTS; PR00171; SUGRTRNSFORT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: TO SUGAR TRANSPORTER FAMILY EMBL; AE003825; AAF58630.1; -- FlyBase; FBgn0033644; CG8234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of Dro
Science 287:2185-2195(2000)
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                                                                                                309
    99
                                                                                                                                                                                                                                                                                                                                   Local
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    EFNSIMEILRPYGAFWLTAAFCILSVLF
                                                                                                                                            HLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 65
                                                                                                HLG--WLPLTCFVIYILGFSLGFGPIPWLMMGEILPAKIRGPAASVVTAFNWFCTFVVTK 366
                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                              Similarity 45.40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00216;
PS00217;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGAR_TRANSPORT_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47357 MW;
                                                                                                                                                                                                                                                                                                                                   43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                              Score 222;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63F0E13046A769DD CRC64;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                              2; DB 5;
4.7e-14;
                                                                                                                                                                                                                                                                                   Indels
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Best Local
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Q9UGQ3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
01-JUN-2001
                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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PRINTS; PR00171; SUGARTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Sugar transport; Transmembrane.
Sugar transport; Transmembrane.
SEQUENCE 507 AA; 54569 MW; 1FC6E2EB11588466
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VU17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doege H., Bocianski A., Joost H.G., Schuermann A.;
"Activity and genomic organization of human glucose transporter (GLUT9), a novel member of the family of sugar-transport facility predominantly expressed in brain and leuccytes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of a sugar transporter gene, a G-beta three novel genes in human chromosome 9q34."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SUGAR TRANSPORTER (GLUCOSE TRANSPORTER 9).
                                                                                                                                                                                                                                 CG10960
                                                                                                                                                                                                                                                                CG10960 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VU17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AJ011372; CAB66155 1; -.
EMBL; Y17803; CAB96996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AFWLTAAFCILSVLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIMGYAVGWGPITWLLMSEVLPLRARGVASGLCVLASWLTAFVLTKSFLPVVSTFGLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR GLUT9
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and genomic o
                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).
(Hordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%;
51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.J., Aziz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                          13,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                        erygota; Diptera; Brachycera; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1FC6E2EB11588460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                         Insecta;
                                                                                                                      Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        facilitators
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RESULT
Q9V609
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dietz S.M.,
RA Fosler C., Gabrielian A., E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A., E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sinh H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhao Q., Zhao Q., Zheng L.,
Science 287:2185-2195(2000)
C. --- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        George R.A., Lewis S.E., KICHARUS S., MINING, Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006: PubMed=10731132:
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goc Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., George R.A., Lewis S.E., Richards S., Ashburner M., H.
    01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AE003540; AAF49874.1; -.
                                            Q9V609
                                                                  094609
                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane.
SEQUENCE 539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGAR_TRANSPORT.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0036316; CG10960.
                                                                                                                                                                        479
                                                                                                                                                                                                                                                 419 VSLGWLPVASLCLFIIMFSIGYGPVPWLMMGELFATDIKGFAGSLAGTSNWLLAFVVTKT 478
                                                                                                                                                                                       67 FNSIMEILRPYGAFWLTAAFCILSVLF 93
                                                                                                                                                                                                                                                                                         7 LGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKE 66
                                                                                                                                                                      FVNLNDGLGIGGTFWLFAGLTVVGVIF 505
                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      58413 MW;
                                                                                                                                                                                                                                                                                                                                                       43.3%;
    13,
13,
                                                                                                                                                                                                                                                                                                                                    18;
Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                   Score 220; DB 5;
Pred. No. 9.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                      A2F4814DBF676BBD CRC64;
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                               489
                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                      Length 539
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                                                                                                                                                                                                                                                                                                                                  Gaps
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RA Burtis K.C. Busam D.A. Butler H. Caddeu E. Center A. Chandra I.,
RA Cherry J.M. Cawley S. Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S. Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Deng Z., Mays A.D., Dew I. Dietz S.M.,
RA Choson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dusbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guah P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T. J., Wei M., H. Diegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Menkov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menkov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G. M., Weissenbach J.,
RA Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Science 287:2185-2195(2000).
                                                                                                                                             Matches
                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, CG7801 PROTEIN. CG7801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i SUBCELLULAR LOCATION: INTEGRAL ME-

-i SIMILARITY: TO SUGAR TRANSPORTER

EMBL, AE003825, AAF58631.1; -

FlyBase; FBgn0033643; CG7801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley Seesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov Sorkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0171; SUGRTRNSPORT PROSITE; PS00216; SUGAR_TRANS
                                                                                                                                                                                                                                                                                                        PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
                                               364
99
                                                                                           6
                                               HLG--WLPLTCFVIYILGFSLGFGPIPWLMMGEILPAKIRGSAASVATAFNWFCTFVVTK 423
                                                                                           HLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.,
                                                                                                                                                                                                                                                                                                                                                                                PF00083; sugar_tr;
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                              53026 MW;
                                                                                                                                                                43.1%;
                                                                                                                                                                                                                                                                                                                                    TRANSPORT_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
                                                                                                                                                              Score 219; DB 5
Pred. No. 1e-13;
                                                                                                                                                                                                                                                              D26436DAD69723C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fly)
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                                                                                                                                             2;
                                                                                                                                          Gaps
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Db

422

| : :||||| | | : : | TFQDLTVAMGAHGAFWLFGAICFVGLFF

449

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RESULT
Q9MAA4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T12H1 genomic s submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.-i- SUBCLIJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY I-SIMILARITY: TO SUGAR TRANSPORTER FAMILY.

EMBL, AC009177; AAR27021.1; --
                                                                                                                                                                                                           Q9V848;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
CG6484 PROTEIN.
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle George R.A., Lewis S.E., Richards S., Ashburner M., Henderso Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.
                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                     Q9V848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
Dfam: DF00083: sugar tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9MAA4
                                                                             STRAIN-BERKELEY;
                                                                                         SEQUENCE FROM
                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
                                                                                                                                                                                               CG6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1
Sugar transport; Transmembrane.
SEQUENCE 463 AA; 50148 MW; 82B93947AE79DAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                          72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                         Created)
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Last annotation update)
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82B93947AE79DAC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200.5; DB 1
No. 6.3e-12;
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                                                                                                                                                                Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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                                                                                                                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnstead M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
   Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 463;
               Henderson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
                                                                                                                                                                  Insecta;
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Q92U87; 01-MAY-1999 01-MAY-1999 01-JUN-2001

9 (TrEMBLrel. 9 (TrEMBLrel. 1 (TrEMBLrel.

10, 10, 17,

, Created) , Last sequence up , Last annotation

Q9ZU87

PRELIMINARY;

PRT;

348

AΑ

Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta;

PUTATIVE SUGAR TRANSPORTER

Spermatophyta;

Magnoliophyta;

eudicotyledons;

core

eudicots;

Embryophyta; Tracheophyta;

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RESULT Q9ZU87 ID Q9 Q9 AC Q9 DI 01 01 DI 01 DI 01 DI 01 DI DI 01 DI FU GN T9 9 OS Ar COC Sp
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rimert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith H.O.,
RA Williams S.M., Woodage T., Worley K.G., Wu D., Yang S., Yao Q.A.,
RA Kimsha S.M., Woodage T., Wolley K., C.,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SUBTAILARITY: TO SUGAR TRANSPORTER FAMILY.
EMBL; AE003802; AAF57829.1;
E1yBase; FBgn0034247; CG6484.
InterPro; IPR003662; sub_transporter.
InterPro; IPR003663; Sugar_transporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
SEQUENCE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00216; SUGAR_TRANSPORT_1; 2. PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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PRINTS; PR00171; SUGRTRNSPORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50271 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                004B4CACF406BDBB CRC64;
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No. 7.5e-11
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Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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\begin{array}{c} \text{AID} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT} \\ \text{DDT
RX MEDLINE=20196006; PubMed=10731132;
RX MEDLINE=20196006; PubMed=10731132;
RA Andams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pielifer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pielifer B.D.,
RA Burandon R.C., Buster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Q9V3G0
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
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pr051TE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Sugar_transport; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; Drosophila.
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les 38; Conserv
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L; AC006072; AAD13706.1; -.
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43.2%;
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Pred. No. 8.9e-11;
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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RA RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradding A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodse T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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InterPro; IPR003663; Sugar_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTTRNSPORT.
PROSITE; PS00215; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
Sugar transport; Transmembrane.
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"Sugar transporters in Drosophila melanogaster.";
"Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
394 PVLNDIIGATACFAIFFGFAVAAFVF 419
                                                                                                                                                       334 GVGWLALIAVCVFIIGFSLGFGPVPWLMMAELFAEDVKALAGSIAGTTNWCFAFIVTLLF 393
                                                                           68
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                                                                                                                                                                                                     GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEF 67
                                                                       NSIMEILRPYGAFWLTAAFCILSVLF 93
                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                            36.6%;
37.2%;
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Pred. No. 1.6e-10;
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gb_pl:BVU43629
gb_htg:AC020266
gb_in:AC011696
gb_htg:ACO17643
gb_htg:ACO10025
gb_htg:ACO19887
gb_in:ACO11252
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gb_in:AEO03601
gb_ba:ABO05554
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gb_in:AC005974
gb_in:AC007414
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gb_pat:AX191497
gb_pat:AX076679
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9b_ro:AB033418
9b_om:AF321324
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gb_in:AE003540
gb_in:AF199486
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gb_in:AE003825
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gb_pr:AL445222
gb_pl:BVU43629
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gb_ro:RNO245935
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Search time (sec): 3231.410000
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-Q=/cgn2_1/USPTO_spool/US09516493/runat_13022002_125123_18437/app_query.fasta_1.
-DB=GenEmbl -QEMP=fastap -SUFFIX=rege -CAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -GAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09516493_eCGNI_1.7057 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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! U43629 Beta vulgaris integral
! AC020266 Drosophila melanoga
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ACO07414 Drosophila melanoga
AEO03831 Drosophila melanoga
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! AE003540 Drosophila melanogas
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AJ245935 Rattus norvegicus mRN
Y17802 Mus musculus mRNA for ç
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1 AC007473 Drosophila melanoga
1 AE003825 Drosophila melanoga
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AX076671 Sequence 5 from Pater
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( AC011252 Drosophila melanoga

( AC008311 Drosophila melanoga

( AE003601 Drosophila melanoga
                                                                                                                                                                                                                                                                                                                                    AC012854 Drosophila melanoga
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alignment_scores:
Quality: 2310.50
Ratio: 5.100
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lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL
                                                                                                                                 heValAlaG1yPheAlaValI]eThrAlaAlaGlnAspValTrpMetLeu
                                                                                                                                                                                 uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProP
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                                                    CTGGGGGGCCGCCTCCTCACCGGCCTGGCCTGCGGTGTTGCCTCCCTAGT
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                                                                  LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa
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Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Reddy, R
Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Yao, M.G.
Gandhi, A.R., Tang, Y.T. and Khan, F.A.
Transporters and ion channels
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/note="Incyte ID No: 1416107CB1"
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                                                                             ValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAl
                                                                                                                                          lyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeu 399
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                                                             GTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGC
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alignment_block: US-09-516-493-7 x HSA245937

seg 1/1 to:

17

73 CGCCGCGTCTTCCTCGCCGCCTTCGCCCGCTGGGCCCACTCAGCTT

122

eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34

ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh

from: 1

to:

1873

Percent Similarity:

Ratio:

2301.50 5.092 99.559

Length: 454
Gaps: 1
Percent Identity: 99.119

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alignment_scores:
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AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol.
20138191
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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glucose transporter; GLUTX1 gene
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                           LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa
                                                                                                                                                                                                                                                                                                                                                                                               euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr 150
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                                                                                                                                                                                                                   GCTTCCTGCTGACTCAGCACAGGCGCCAGGAGGCCATGGCCGCCCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                 TCGGCTCCTGTGTGCAGCTAATGGTCGTCGTCGGCATCCTCCTGGCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCCCGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGC
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SOURCE
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                                                                                              Loases 1 to 1508)

Doege, H., Schurmann, A., Bahrenberg, G., Brauers, A. and Joo GLUT8, a novel member of the sugar transport facilitator with glucose transport activity

J. Biol. Chem. 275 (21), 16275-16200
Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057 Aachen, FRG
                                                    Direct Submission
                                                                   2 (bases 1 to 1508)
Joost, H.G.
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                 glucose transporter
                                                                                                                                                                                                                                                                                Y17801.1 GI:7688145
                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA
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for glucose transporter 8
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gene)
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alignment_block: US-09-516-493-7 \times HSA17801
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Quality: 2298.50
Ratio: 5,085
Percent Similarity: 99.559
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151 LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa 167
                                                                                                                                                                                                                                 296 GGTGGACCGCCGGGCGCAAGCTGAGCCTCTTGCTGTGCTCCGTGCCCT
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                            TCGGCTCCTGTGCAGCTAATGGTCGTCGTCGGCATCCTCCTGGCCTAC
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27. .1460
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27. .1460
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/db_xref≔"taxon:9606"
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Gaps:
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449	heCysValProGluThrLysGlyLysThrLeuGluGlnIleThrAlaHis	433
1445		1396
433	aPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuP	416
1395		1346
416	ValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAl	400
1345		1296
399	lyValalaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeu	383
1295		1246
383	yProIleProTrpLeuLeuMetSerGluIlePheProLeuHisValLysG	366
1245		1196
366	AlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGl	350
1195		1146
349 1145	laProvalSerAlaGlnProvalAspAlaSerValGlyLeuAlaTrpLeu	333 1096
333 1095	eLysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerA	316 1046
316	LeuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPh	300
1045		996
299	laValalaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuVal	283
995		946
283	pSerSerLeuAlaSerValValValGlyVallleGlnValLeuPheThrA	266
945		896
266	AlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLysAs	250
895		846
249	helleIleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsn	233
845		796
233	uGlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProP	216
795		746
216 745	PheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGl	200 696
199 695	rgPheLeuLeuThrGlnHisArgArgGlnGluAlaIleAlaLeuArg	184 646
184	lProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrProA	167
645		596
595	TIGCAGGCTGGTGCTGGAGTGGCGCTGGCTGTGCTGGCTGGC	546

450 PheGluGlyArg

1446 TTTGAGGGGCGA 1457

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alignment_block:
US-09-516-493-7 x AX076669
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AUTHORS
TITLE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 2057.00
Ratio: 4.633
Percent Similarity: 97.582
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LOCUS AX076669
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thorens,B., Ibberson,M. and Uldry,M. Glutx polypeptide family and nucleic acids encoding same Patent: WO 0104115-A 3 1B-JAN-2001; University of Lausanne (CH)
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LSVLFTLTFVPETKGRTLEQITAHFEGR"

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/db_xref="taxon:10118"
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98	382 ysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPhe 3	(4)
82 248	365 pGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisvall 3	Ε
65 198	349 LeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTr 3 	Н
48 148	332 erAlaProValSerAlaGlnProValAspAlaSerValGlyLeuAlaTrp 3 :::   :::    :::   :::   :::   ::: 1099 TGGTGCCCATCTCCGCAGAGCCTGCTGATGTTCACCTGGGGCTGGCCTGG 1	ш
.098	315 rPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleS 3	<u> </u>
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398	:::	

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GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne CH-1005, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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IFWLLMSEIFPLHIKGVATGVCVTTNNFMAFLYTKEFNSIMEILRPYGAFWLTAAAFGI
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                                                                                                                                                               Doege,H., Schurmann,A., Bahrenberg,G., Brauers,A. and Joc GLUTB, a novel member of the sugar transport facilitator with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                            Direct Submission
Submitted (16-JUL-1998) H. Joost,
Toxicology, Technical University
Aachen, FRG
                                                                                                                                                                                                                                                                                                              Y17802.1 GI:7688219
glucose transporter 8; GLUT8 gene
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for glucose transporter
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                                                                                  Aachen, Wendlingweg 2, D-52057
                                                                                                    Institute of Pharmacology and
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alignment_block:
US-09-516-493-7 x MMU17802
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                                                      LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa
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US-09-516-493-7 x AF232061
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                                                          AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe
uValAspArgAlaGlyArgLysLeuSerLeuLeuCysSerValProP
                                      CCGCACCCCGGCCCTGCGCCTCGGAGACAATGCGGCCTCCTGGTTCGGG
                                                                                                                                                                                         CGGCTTCGCGCTCGGCTACAGCTCCCCCGCCATCCCCAGCCTGCGGCGCA
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Carayannopoulos, M.O., Chi, M.M., Cui, Y., Pingsterhaus, J.M., McKnight, R.A., Mueckler, M., Devaskar, S.U. and Moley, K.H.
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MAALRFLWGSBEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
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SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGICVLTNWEMAFLVTKEFSSVMEMLRPYGAFWLTAAECAL
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/strain="129"
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Thorens,B., Ibberson,M. and Uldry,M. Glutx polypeptide family and nucleic Patent: WO 0104145-A 5 18 JAN-2001;
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                                                                                                                                                                                                                                                                                                         /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                            organism="Mus sp."
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alignment_block: US-09-516-493-7 x AX076671

Percent Similarity:

Align seg 1/1 to: AX076671

from:

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to:

2072

ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh

alignment_scores:

Quality:

Ratio:

: 2041.50 : 4.608 : 97.363

Percent Identity: 85.934

Length: Gaps:

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                                                                                                                                          SASpSerSerLeuAlaSerValValValGlyValI1eGlnValLeuPheT
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GCCTTGTCGGGTGTGATCATGGTGTTCAGTATGAGTGCCTTTGGTACCTA
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SOURCE
ORGANISM
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LOCUS MMU245936
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                                                                                                                                                                                                  Direct Submission Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne CH-1005, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                  Ibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucose transporter; GLUTX1 gene.
house mouse.
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      uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProP

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      |cctggAccgttcagggcgcaAggctgaggcttttgctcttgcaccgtgcccttt

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                                  GTTTTCTCCTCACTCAACACCAGTACCAGGAGGCCATGGCTGCCTTGCGC
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PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL
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                                                                                                                                                                              CATTTCGAGGGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACCCATCCCCTGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCA
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glucose transporter
Rattus norvegicus cl
Rattus norvegicus
                                                                                       Rattus norvegicus
                                           AB033418.1 GI:7592743
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glut8
                CDNA
                ţ
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                mRNA,
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                clone_lib:testis
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ORGANISM

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AB033418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                   378
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                                                                                                                                                       328
                                                                                                                                                                                                                                      278 CCGCACCCCTGCCCTACGCCTCGGAGACACTGCGGCCTCCTGGTTCGGG
                                                                                                                                                                                                                                                                                                                            228 CGGCTTCGCGCTTGGCTACAGCTCCCCCGCCATCCCCAGCCTGCGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                178 CGCCGGGTCTTCCTTGCCACCTTCGCCGCCCGCCCTCGGCCCCCTCAGCTT
                        83
                                                                                                                                                                       51 AlaValValThrLeuGlyAlaAlaAla...GlyGlyValLeuGlyGlyTr 66
                                                                                                                                                                                                                                                                               34 laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly
                                                                                                                                                                                                                                                                                                                                                   17 eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34
                                                               roPheValAlaGlyPheAlaValfleThrAlaAlaGlnAspValTrpMet
                                                                                                                                                     GCCGTCGTGACCCTGGGCGCCTGCGGCCCAGGGGGCCCGTGCTGGGGCGCCTG
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Quality: 2040.50
Ratio: 4.596
milarity: 97.368
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Ishibashi,K.
Direct ""
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Molecular cloning of a new putative glucose transporter Published Only in DataBase (2000) In press
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109. .1
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1 702 c 609 g 486 t
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Gaps: 3
Percent Identity: 85.307
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                        99
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1327		1278
364	TrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGl	348
1277		1228
347 1227	leSerAlaProValSerAlaGlnProValAspAlaSerValGlyLeuAla ::::   :::      :::    :::   ::: TCCTGGTGCCCATCTCCGCAGAGCCTGCTGATGTTCACCTGGGGCTGGCC	331 1178
331 1177	aTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHisvalAlaI :                   :::       :::  CTACTTCAAACTGACCCAGAGTGGCCCCAGCAACTCCCCCCATGTAGGCC	31 <b>4</b> 1128
314 1127	LeuValLeuSerGlyValValMetValPheSerThrSerAlaPheGlyAl     :::           :::               CTGGCCTTGTCGGGTGTGATCATGGTTTTCAGCATGAGCGCCTTTGGTAC	298 1078
297	heThralaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeu	281
1077		1028
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977	:::          :::	928
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777		728
183	SValProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrP	166
727	:::                  :::	678
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677	:::	628
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627		578
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577		528
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477	CCTTCGTGACCGGTTTTGCTGTCATCACCGCGGCCCGGGGATGTGTGGATG	428

102

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alignment_block:
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ORIGIN
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AUTHORS
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Source
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KEYWORDS
                                                                                  Align seg 1/1 to: AF321324
                                                                                                                 US-09-516-493-7 x AF321324
                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_om:AF321324
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                     122 IleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCysVa 138
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ATCTCGGAAATCGCCTACCCTGAGGTGCGAGGGCTGCTCGGCTCCTGTGT 50
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                                                                                                                                                                         Quality: 1519.00
Ratio: 4.732
milarity: 96.108
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-NOV-2000) Anatomy and Cell Biology, Medicine, Martin Luther University Halle, Grosse; Halle 061097, Germany
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AF321324
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/db_xref="taxon:9913"
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oGluThrLysGlyLysThrLeuGluGlnIleThrAlaHisPheGluGlyA 453
                                                                                                                                     CGGCGTCTGCGTCCTCACCAACTGGTTCATGGCCTTTCTGGTGACCAAAG
                          GCCTCTGCCTTCTGCATCTTCGGTGTCCTTTTCACTCTGGCCTGTGTCCC
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                                                                                                                                                     TGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCCAC
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Quality: 1427.00
Ratio: 4.725
Percent Similarity: 66.374
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US-09-516-493-7 x AX191507
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LOCUS AX191507
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  330
                                                                              280
                                                                                                   51 AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe 67
                                                                                                                                                              230 CCGCGCCCCGGCCCGCGCCTGGACGACGCCGCCGCCTCCTGGTTCGGG
                   67 uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProP 84
                                                                                                                                                                                 34 laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly 50
                                                                              GCTGTCGTGACCCTGGGTGCCGCGGCGGGGGGGGGGGGTGCTGGCT 329
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GGTGGACCGCGCGCGCGCAAGCTGAGCCTCTTGCTGTGCTCCGTGCCCT 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1461)
Kato,S. and Kimura,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29 from Patent W00149728. AX191507
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61. .849
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CSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYTSETAYPAVRGLLGSC
VQLMVVVGTLLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA
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/db_xref="GI:15209698"
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Gaps: 4
Percent Identity: 66.154
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0	ValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeuV	œ
911		911
383	roTleProTrpLeuLeuMetSerGlullePheProLeuHisValLysGl	O.
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366	ValGlySerMetCysLeuPheIleAlaGly.PheAlaValGlyT	350
7	ValSerAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeu 	
	CTGACCCAGGGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGC	
333		$\vdash$
317 776	yValValMetValPheSerThrSerAlaPheGlyAlaTy 	300 727
	CTGGTCT	
300	lAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuLeuVal	284
718		718
283	Ser Leu Ala Ser Val Val Val Gly Val I le Gln Val Leu Phe Thr A	
718		$\rightarrow$
267	alMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLysAs	
718		$\vdash$
250	$. Le {\tt IleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnA}$	234
233	$. Ser {\tt PheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProPlant} \\$	217
718		
217	.euTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGlu	200
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200	gPheLeuLeuThrGlnHisArgArgGlnGluAla.IleAlaLeu	8
184 679	roSerLeuMetLeuLeuLeuMetCysPheMetProGl 	167 630
167 629	AlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCy 	
150 579	:lySerCysValGlnLeuMetValValValQlyIleLeuLeuAlaT 	
	aProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLe 	117 480
117 479	uGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeu 	ωο
100	ALAGLYPheAlaValIleThrAlaAlaGlnAspVa 	380

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FEATURES
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US-09-516-493-7 x AX191497
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Percent Similarity:
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                                        uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProp 84
                                                                                                 CCGCGCCCCGGGCCCGCGCCTGGACGACGCCGCCGCCTCCTGGTTCGGG
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Ratio: 4.772
nilarity: 70.088
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Kato,S. and Kimura,T.
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Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
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Eukaryota; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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296 c 259 g 15
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Gaps: 2
Percent Identity: 69.795
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                                                                                                                                                              uSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPheL
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DEFINITION ACCESSION VERSION

...../9 2011 bp E N Sequence 13 from Patent W AX076679 AX076679.1 GI:1271777

DNA WO0104145.

PAT

06-FEB-2001

seq_documentation_block: LOCUS AX076679

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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US-09-516-493-7 x AX076679
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ORIGIN
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117 lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 134
                                                                     409
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                                                                                                                                                          359 CGGCCATTGGCTATGCACTCATGGCTGGCCGTGGCCCTCTGGATGCTT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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IPLLATMLFIMGYANGWGPTTWILLMSEVLPLRARGVASGLCVLVSWLTAFVLTKYFLL
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200 705	b	184 659
184 658		167 609
167 608		151 559
150 558	euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr      ::: 	134 509
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+ 2310.50 3829.30
+ 2301.50 3813.61
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and

preventing transport,

Novel human transporter and ion channel proteins useful for treating

neurological,

muscle and

immunological

Tang

Khan FA; Burford N,

JL,

Azimzai Y,

Au-Young Yue H,

J, Lu Nguyen

Yao MG,

Gandhi

Lal

(INCY-) INCYTE GENOMICS

P-PSDB;

2001-418042/44. AAE04888

TRICH is near

Claim 5; disorders

Page 140-141; 160pp; English.

The present sequence is transporter and ion channel (TRICH-1) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipola

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD09552
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/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV11474
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC35123
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC35261
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAK53274
28-JAN-2000;
02-FEB-2000;
10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; disease; cerebral neoplasm; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
                                                              21-JAN-2000;
                                                                                                                                                                                                                    WO200146258-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          demyelinating disease; mental disorder; Schizophrenia; polymyositis;
muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human transporter and ion channel-1 (TRICH-1) cDNA.
                                                                               14-JAN-2000;
                                                                                                   23-DEC-1999;
                                                                                                                                       22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                             malabsorption
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99US-0172000.
2000US-0176083.
2000US-0177332.
2000US-0178572.
2000US-0179758.
2000US-0181625.
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                                                                                                                                       2000WO-US35095
                                                                                                                                                                                                                                                                                                                                                                                             syndrome; hypercholesterolaemia; cancer; ss.
                                                                                                                                                                                                                                                                         Location/Qualifiers
46.1479
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                                                                                                                                                                                                                                                         "Human TRICH-1 protein"
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alignment_block:
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                                                             167
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                                                                                                                                                                                                                                                                                                              465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
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                                                                                                                             LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa 167
                                                                                                                                                                                                                         euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr 150
GCCCCCTCCCTCATGCTGCTTCTCATGTGCTTCATGCCCGAGACCCCGC
                                           lProProSerLeuMetLeuLeuMetCysPheMetProGluThrProA 184
                                                                                                 GGCCCCGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGC
                                                                                                                                                                                                                                                                                                                        lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 134
                                                                                                                                                                                                                                                                                                                                                                                           CTGGGGGGCCCCCCCCCCCCGGCCTGGCCTGCGGTGTTGCCTCCCTAGT
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ID AAF55865 standard;
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AAF55865 standard; cDNA;

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55865

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                     PheGluGlyArg 453
                                                                                         heCysValProGluThrLysGlyLysThrLeuGluGlnIleThrAlaHis 449
TTTGAGGGGCGA 1476
                                                                                                                                   CTTCTGGCTTGCCTCCGCTTTCTGCATCTTCAGTGTCCTTTTCACTTTGT
                                                                                                                                                       aPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuP
                                                                  TCTGTGTCCCTGAAACTAAAGGAAAGACTCTGGAACAAATCACAGCCCAT
                                                                                                                                                                                                                      ValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAl
                                                                                                                                                                                                                                                                        GCGTGGCGACAGGCATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCTC
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27 - AUG-1999;
23 - FEB - 2000;
                                                                                                                                                                                                                                                                                                       417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
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GCTGTCGTGACCCTGGGTGCCGCGGGGGGGGGGGGAGTGCTGGCCT
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DB; AAB66932.
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               AlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpG1
                                                            CAAGCTGACCCAGGGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGG
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Sequence

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seq_documentation_block:
IID AAF55866 standard; cb
XX AAF55866;
XX AAF55866;
XX DT 17-APR-2001 (first e
DE Rat GLUTX1 coding seq
XX Rat; GLUTX; gene then
KW hexose transport disc
KW hypoglycaemia; gluco;
OS Rattus sp.
YX W0200104145-A2.
YX 18-JAN-2001.
YX 18-JAN-2001.
YX 14-JUL-1999; 99US-
PR 14-JUL-1999; 99US-
PR 14-JUL-1999; 29US-
PR 13-JUL-2000; 2000WO-
XX PD 14-JUL-1999; 99US-
PR 13-JUL-2000; 2000WS-
YX W020010411-112615/12
PR 13-JUL-2000; 2000US-
YX WPI; 2001-112615/12
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                                                        The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a
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                neurodegenerative disease. The present sequence for rat GLUTX1.
                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHisValALaIleS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnAlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLy
                                                                                                                                                                                                                                                                                                                                                                               2072 BP
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18-JAN-2001

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alignment_block: US-09-516-493-7 \times AAF55867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAF55867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2072 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 73-74; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB66934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLA-) UNIV LAUSANNE
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                                                                                                                    84
                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                       34 laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly ::||||||||||||
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                                                                                                      heValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMetLeu
                                                                                                                                                                                                                           AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe
                                                                                                                                                                                                                                                                      CCGCACCCCGGCCCTGCGCCCTCGGAGACAATGCGGCCTCCTGGTTCGGG
                                                                                                                                                                                                                                                                                                                                lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL
                            CTCGGAGGCCGCCTCCTCACCGGCCTTGCCTGCGGAGTCGCCTCACTAGT
                                                                                        TCGTGACTGGCTTTGCTGTCATCACCGCGGCCCGGGATGTGTGGATGCTG
                                                                                                                                                  CCTGGACCGTTCAGGGCGCAAGCTGAGCCTCTTGCTCTGCACCGTGCCCT
                                                                                                                                                                  eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA
                                                                                                                                                                                                                                                                                                                                                                                              CGCCGGGTCTTCCTTCGCTTCGCCGCCGCTCTGGGACCCCTCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine GLUTX1
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2000US-0184285.
2000US-0616132.
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4.608
97.363
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85.934
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and

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                                    yAlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrL
                                                                            CTAGTGACCAAAGAGTTCAACAGCGTCATGGAGATGCTCAGACCCTACGG
                                                                                                  LeuValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGl
                                                                                                                                                                                     ysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPhe
                                                                                                                                                                                                                                                 GGGACCCATCCCCTGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCA
                                                                                                                                                                                                                                                                    pGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisValL
                                                                                                                                                                                                                                                                                                                                CTGGCTGTAGGCAGCATGTGCCTCTTCATTGCTGGCTTTGCGGTGGGCTG
                                                                                                                                                                                                                                                                                                                                                   LeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTr 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                      er \verb|AlaProValSerAlaGlnProValAspAlaSerValGlyLeuAlaTrp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTTGTCGGGTGTGATCATGGTGTTCAGTATGAGTGCCTTTGGTACCTA
TGCCTTCTGGCTCACCGCTGCCTTCTGCGCTCTCAGTGTCCTATTCACAC
                                                                                                                                                              AGGGTGTGGCTACCGGCATCTGTGTCCTCACCAACTGGTTCATGGCCTTT
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hrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuLeu

298 939 282 889 265 839 248 789 232

CTGCTGTGGCGCCCTCATCATGGACAGAGCAGGGCGAAGGCTGCTCCTG

265 840 249

SASpSerSerLeuAlaSerValValValGlyValIleGlnValLeuPheT

AATGCTATCATGTTCTATGCCAACAGCATCTTCGAGGAGGCCAAGTTCAA AsnAlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLy CCCTCATCATCGGCATTTCCCTCATGGTCTTCCAGCAGCTGTCAGGGGTC roPheIleIleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyVal GCACCAGGGCTTCCAGCTGGCCCTGCTGAGGCGCCCTGGCATCTACAAGC

GGACAGCAGCCTGGCCTCGGTCACTGTGGGCATAATCCAGGTCCTGTTCA

740 216

790

640

184

200

TTCCTGTGGGGCTCTGAGGAGGGCTGGGAAGAGCCCCCTGTTGGGGGCTGA PheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGl rgPheLeuLeuThrGlnHisArgArgGlnGluAlaIle...AlaLeuArg

216 689 199 639 184

.GlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysP

590

167

| ProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrProA GTGGCAGGCTGGGTCCTAGAGTGGCGCTGGCTGGCCGTGCTGGGCTGTGT LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa TCGGCTCCTGTGCAGCTGATGGTTGTCACTGGCATCCTCCTGGCCTAT euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr GGCACCGGTTTACATCTCGGAAATCGCCTACCCAGCTGTCCGAGGACTGC

167 539

589

GCCCCCCACCCTCATGCTGCTCATGTGCTACATGCCCGAGACCCCAC

540

490

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seq_documentation_block:
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                                                                                                                                                                                                                                                             06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
                                                                                                                                                                                                      Kato
                                                                                                                                                                                                                        (PROT-)
(SAGA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449
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                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoiesis; tissue growth activity; Parkinson's disease; cytostat
Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
                                                                                                                                                                                                                                                     03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                    WO200149728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 contraceptive; antiinfertility; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein having hydrophobic domain encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD12574 standard;
                                                                                                                                                                                                                                                                                                             28-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTTCGAGGGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisPheGluGlyArg 453
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                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydrophobic domain;
                                                                                                                                                                        AAE06579
                                                                                                                                                                                                                         SAGAMI
                                                                                                                                                                                                                                  PROTEGENE INC
                                                                                                                                                                                                      Kimura
                                                                                                                                                                                                                                                    ; 2000JP-0002299.
; 2000JP-0026862.
; 2000JP-0058367.
                                                                                                                                                                                                                                                                                2000JP-0000585
2000JP-0000588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                         CHEM
                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Human protein having hydrophobic domai
/note= "CDS is specifically is claimed in claim ?
                                                                                                                                                                                                                                                                                                                                                                                                    61..849
                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA; 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA clone HP10784.
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Human proteins with hydrophobic domains and the nucleic acids er them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's useful for preventing diagnosing imer's and inflammation encoding

Claim 4; Page 287-289; 563pp; English.

The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodia and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional antibodies

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alignment_block:
US-09-516-493-7 x AAD12574
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                              530
                                                                                                                                                                                                                                                                                                                                                                                                                           480
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                                                                                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 heValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMetLeu 100

    uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProP

    |||||||||||||||||||||||

    GGTGGACCGCGCGCGCGCCAAGCTGAGCCTCTTGCTGCTGCTCCGTGCCCT

                                                                      rgPheLeuLeuThrGlnHisArgArgGlnGluAla.IleAlaLeuArgPh
                                                                                                                                       CGCCGCGTCTTCCTCGCCGCCTTCGCCGCCTGCGCCCCACTCAGCTT 179
eLeuTrpGlySerGluGlnGlyTrpGluAspProPro1leGlyAlaGluG
                                                                                                                                                                                     1ProProSerLeuMetLeuLeuMetCysPheMetProGluThrProA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGGGGCCCCCCCCCCCCCGCCCTGGCCTGCGGTTGCCTCCCTAGT 479
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                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCCCGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1427.00
Ratio: 4.725
milarity: 66.374
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Gaps: 4
Percent Identity: 66.154
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71	: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF5587	seq_name:
	GAGGGGCG	1030
	⊏	450
450 1029	eCysValProGluThrLysGlyLysThrLeuGluGlnIleThrAlaHisP 	433 980
7	TICTGGCTTGCCTCCGCTTTCTGCATCTTCAGTGTCCTTTTCACTTTGTT	w
433	he Trp Leu Ala Ser Ala Phe Cys Ile Phe Ser Val Leu Phe Thr Leu Van Leu Phe Thr Leu Van Van Van Van Van Van Van Van Van Van	417
929	CTCAGGCCCTATGGAGCC	912
416	erLeuMetGluValLeuArgProTyrGlyAl	400
911		911
400	hr GlyIleCysValLeuThrAsnTrpLeuMetAlaPhe	383
911		911
383	uIlePheProLeuHisV	367
911	GGGCAGCATGTGCCTCTTCATCGCCGGA	877
366	ValGlySerMetCysLeuPheIleAl	350
876	CCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGGCTGGCCTGGCTGG	N C
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333 826	ysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerAla 	317 777
776	TCAGGTGTGTCATGGTGTTCAGCACGAGTGCCTTCGGCGCCTACTTC	727
317	uSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPheL	300
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300	.aAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuV	284
718		718
283	yValIleGln	267
718		718
267	${\tt rAlaGluThrIlePheGluGluAlaLy}$	250
718		718
250	Ile Ile Gly Val Ser Leu Met Ala Phe Gln Gln Leu Ser Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly Val Asn Alander Gly	234
718		718
233	$In Ser {\tt PheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProPhe}$	217
718		718

seq_documentation_block:
ID AAF55871 standard; cf
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AC AAF55871;
XX
DT 17-APR-2001 (first e
XX
DT 17-APR-2001 coding sec

Rat GLUTX3 coding sequence

(first entry)

CDNA; 2011 BP

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alignment_scores:
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    Ratio:
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US-09-516-493-7 x AAF55871
                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAF55871
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
309 CAATGACCTCTTGGGCCGGAAGCTCAGCATCATGTTTTCCGCTGTCCCCT 358
                                                                    259
                                                                                                                         209 CTTCTGACCCAGCACTACGCCTGGACAAAATCCAGGCATCCTGGTTTGGG
                                                                                                                                                                                              159
                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUTI-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2011 BP; 337 A; 621 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                  67
                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1999; 99US-0143907.
27-AUG-1999; 99US-0151140.
23-FEB-2000; 2000US-0184285.
13-JUL-2000; 2000US-0616132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYLA-) UNIV LAUSANNE
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                                                                                                                                                                                                                                                                       1 ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh 17•
                  uValAspArgAlaGlyArgLysLeuSerLeuLeuCysSerValProp 84
                                                                              TGGGTATGCCCTGGTCTACACATCTCCAGTCATCCCTGCGCTGAAGCGCT 208
                                                                                                                                           laAlaProProAlaProArgLeuAspAspAlaAlaSerTrpPheGly 50
                                                                                                                                                                                                        eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34
                                                             TCCGTGTTCACCCTGGGTGCCGCCGCCTGGGGGCCTCAGTGCTATGCTACT
                                                                                                                                                                                                                                                       AGAAGGGTGTTCCTGGCCACCTTCGCTGCCGTGCTGGGCAATTTCAGCTT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-112615/12.
DB; AAB66938.
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Gaps:
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389	373 etSerGluIlePheProLeuHisValLysGlyValAlaThrGlyIleCys :	
373 1255	56 uPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuM	
356 1205	0 ValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCysLe::::::::::::::::::::::::::::::::::::	
339 1155	nSerSerHisValAlaIleSerAlaProValSerAlaGlnPro :::: :::::::::         CACTGTGGAGATCGTGACGCTTGGGGGCACGGAGCAGCCCCA	11 3
323 1105	08 rThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyP::::::::::::::::::::::::::::::::::::	10
308 1055	'alValMetValPheSe :::    CCATTATGTTTGTCGC	10
291 1005	75 lyValIleGlnValLeuPheThr/   :::::::::    ::: 56 GTGCTGTGAGGCTCCTGTCTGTG	(0 N)
275 955	heLysAspSerSerLeuA     ::: TGCTGCCCTCCCAGCAGG	10 N
259 905	ValAsnAlaValMet :::: ATCACTCCCATCCTC	m N
242 855	26 lnProGlyIleTyrLysProPheIleIleGlyValSerLeuMetA ::    :::   :::            6 AGCCCCGTGTGTACCGGCCTATTCTCATTACAGTGCTGATGCGTT	~ N
226 805	AlaGluGlnSerPheHisLeuAlaL :::       ::::::: aACGTGCGGAGACAGAGTAGCCGAGTGTCGT	. 1 . 11
214 755	uTrpGlySerGluGlnGlyTrpGluAspProp       	
200 705	184 rgPheLeuLeuThrGlnHisArgArgGlnGluAlaIleAlaLeuArgPhe	
184 658	roProSerLeuMetLeuLeuLeuMetCy    	
167 608	AlaGlyTrpValLeuc     ;::     CTTGGTCTTCTGCTGC	
150 558	ValValValGlyIleLeuL :::            GCCGTGTTTGGATCCCTGT	
134 508	117 lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 	
117 458	1 LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValA               :::        :::	
100	G D	

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seq_documentation_block:
ID AAF55870 standard; cDNA; 1541 BP
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                                             The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTX3.
                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disorce.g. is chemia and diabetes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390
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23-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human GLUTX3 coding sequence
Sequence 1541 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypoglycaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
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                                                                                                                                                                                                                                                                               3; Page 81-82; 124pp; English.
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2000US-0184285.
2000US-0616132.
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alignment_scores:

alignment_block: Align seg 1/1 to: AAF55870 US-09-516-493-7 x AAF55870 316 116 134 266 216 866 CAGCAGCTGACGGGCATCACGCCCATCCTGGTCTACCTGCAGTCCATCTT 466 CATCCCGGTGTACGTGTCTGAGATTGCTCCCCCAGGCGTTCGTGGGGCTC 515 101 366 84 67 51 17 34 laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly rgPheLeuLeuThrGlnHisArgArgGlnGluAlaIle...AlaLeuArg 199 lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 134 LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa AAAAGGGTGTTCCTGGCCACCTTCGCCGCAGTGCTCGGCAATTTCAGCTT Similarity: GlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGluThrIlePh CCCCCCACGTGTGCCGGCCCATCACCGTGGCCTTGCTGATGCGCCTCCTG lnProGlyIleTyrLysProPheIleIleGlyValSerLeuMetAlaPhe GGACAACGTCCGGAGACAGAGCAGCCGAGTATCGTGGGCTGAGGCACGGG y.....AlaGluGlnSerPheHisLeu.....AlaLeuLeuArgG TGCCTGCGTGGGACGGACGTCGATGTCCACTGGGAGTTCGGGCAGATCCA 765 PheLeuTrpGlySerGluGlnGly.....TrpGluAspProProIleGl 214 GCTTCCTGCTCTCGGGGCAGGGACGAAGAGGCCCTGCGGGCGCTGGCC GCCTGTGCTCATCATGATCCTGCTGCTCAGCTTCATGCCCAACTCGCCGC GCCCTTGGCCTCCTGCCGTGGCGGCTGGCTGGCTGTGGCCGGGNAGGC LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa 167 TGGGGGCCACACCCCAGCTCATGGCAGTGTTCGGATCCCTGTCCCTCTAC euGlySerCysValGlnLeuMetValValValGlyTleLeuLeuAlaTyr CTGCTCGGAAGGACGCTGACGGGCTTCGCCGGGGGGGCTCACAGCTGCNTG 465 CGGCGGCCGGCTATGCGGTCATGGCGGGTGCGCACGGCCTCTGGATGCTG heValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMetLeu 100 TCCGTGTTCACCCTGGGAGCAGCGGCGGAGGCCTGAGTGCCATGATCCT AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe CCTTGGATCCTGACCTGCATCTGACCAAATCCCAGGCATCCTGGTTTGGG TGGGTATGCCCTGGTCTACACATCCCCTGTCATCCCAGCCCTGGAGCGCT eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA Arg Arg Val Phe Leu Ala Ala Phe Ala Ala Ala Leu Gly Pro Leu Ser Phenomen Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the ControRatio: 928.00 2.737 71.519 from: Percent ب Identity: . : 1541 Gaps: 45.570 915 865 815 226 150 415 215 34 165 242 715 665 615 565 365 84 315 67

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ID AAC36319 standard; DN
XX
AC AAC36319;
XX
I7-OCT-2000 (first e
XX
DF Arabidopsis thaliana
XX
KW Hybridisation assay;
KW protein identificatio
KW protein identificatio
KW metabolic pathway; pr
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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                                                                                                                                                Claim 7; Page 78; 87pp; English.
                                                                                                                                                                               Human TRANP coding sequences,
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P-PSDB; AAY31639.
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Hillman JL,
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                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                 05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transport-associated protein; TRANP; nuclear pore; nuclear transport; vesicle trafficking; cancer; cystic fibrosis; multidrug resistance; hypercholesterolaemia; diagnosis; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ11731;
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Lal P, Yue
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/product= "Human transport-associated protein-1"
                                                                                                                                                                                                                                     Baughn MR, Corley NC, H;
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This sequence represents human transport-associated protein-1 (TRANP-1) CDNA. The DNA sequence was first identified in a human colon tissue cDNA library. The full-length cDNA was derived from a series of overlapping and/or extended cDNA sequences and is a consensus. TRANP-1 to 9 (AAY31639-Y31647) are a novel group of proteins with chemical and structural homology that are involved in molecular transport. Various disorders are associated with defects in the transport of molecules, either intracellularly or to the extracellular environment. Examples of such disorders include cystic fibrosis, multidrug resistance, hypercholesterotaemia and certain forms of diabetes mellitus. Defective nuclear transport may play a role in cancer. For example, the BRCA1 protein, associated with familial breast cancer, is normally imported into the nucleus via nuclear pore complexes, but is

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alignment_block:
US-09-516-493-7 x AAZ11731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noradrenaline, leading to hypertension. TRANP is expressed in cells, and transport disorders result from either excessive or insufficient molecular transport. Anti-TRANP antibodies and number of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aberrantly located in the cytoplasm in breast cancer cells. In other cancers, cells can secrete excessive amounts of hormones e.g. cancer the adrenal medulla can secrete excessive amounts of adrenaline and noradrenaline, leading to hypertension. TRANP is expressed in cancer
184 rgPheLeuLeuThrGlnHisArgArgGlnGluAlaIle..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 CAACGACCTCCTGGGCCGGAAGCTGAGCATCATGTTCTCAGCTGTGCCGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1527 BP; 216 A; 519 C; 494 G; 298 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a a TRANP antisense nucleotide can be used to treat cancers. A TRANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agonist or expression vector may be used to treat a disorder caused by reduced transport of biologically active molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 heValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMetLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 uValAspArgAlaGlyArgLysLeuSerLeuLeuCeuCysSerValProp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh
                                                                                                                                                                                                                                                 LeuGlyGlyArgLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa
                                                                                                                                                                           GCCTGTGCTCATCATGATCCTGCTGCTCAGCTTCATGCCCAACTCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                           GCCCTTGGCCTCCTGCTGCCGTGGCGGCTGGCTGTGGCCGGGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGGGCCACCCCCAGCTCATGGCAGTGTTCGGATCCCTGTCCCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCCCGGTGTACGTGTCTGAGATTGCTCCCCCAGGCGTTCGTGGGGGCTC 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCGGCCGGCTATGCGCTCATGGCGGGCTGCGCACGGCCTCTGGATGCTG
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.AlaLeuArg 199
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	e 388 : A 1509	388 1509
388 1508	euMetSerGluIlePheProLeuHisVal.LysGlyValAlaThrGlyIl 	372 1462
372 1461	uPhelleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuL  ::::::       :::	356 1413
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351 1312	ValGlyLeuAla.TrpLeuAlaV         :::::          GTAGGTGTGGTGGTGGCTCAGAGGGGCAGGCTGTCTTGGGTGTTAAGGGA	344 1263
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333 1162	GlyProGlyAsnSerSerHisValAlaIleSerAl	322 1113
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305 1068	MetAspArgAlaGlyArgArgLeuLeuVealLeuSerGlyValVealMe                   :::::       :::       	289 1019
288 1018	alvalValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeuIle	272 969
272 968	eGluGluAlaLysPheLysAspSerSerLeuAlaSerV  ::::::::        :::::::  cgaCAGCACCGCTGTCCTGCCTGCCCCCAAGGACGACGCAG	259 928
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAGAAATATGGTCGATCTGTCATCATTGGTGTTTCCCTGATGGTATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlyS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAGGTTCTTTACAGGATATGGAATTGGAGTTTTTTCTTATGTGGTCCC
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                                                                                                                                                                                                                                                                                                                                                                  GlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGluThrIlePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGGAAAAGATGCAGATATCACAAATGAAGCAGACGGTATTCAAGTCTC
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                                                                                                                                                                                        GACAGAGCCGGAAGAAAACCATTGCTACTGGTTTCTGCAACAGGGTTAGT
                                                                                                                                           AspArgAlaGlyArgArgLeuLeuLeuValLeuSer.....GlyValVa
                                                                                                                                                                                                               alValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeuIleMet
                                                                                                                                                                                                                                                          CTCGATATTTGAGCAAGCAGGTTTT...CCCACAAGACTTGGGATGATAA
                                                                                                                                                                                                                                                                               CCAGGATTATATCGAAACTCTGGAAAGGCTACCGAAAGCCAAGATGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nSerPheHisLeuAlaLeuLeuArg.....
                                                                                  {\tt lMetValPheSerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnG}
                                                                                                                                                                                                                                                                                                                              ATGGTGTTTCAGCAGTTTGGAGGAATCAACGGAATATGTTTCTACACAAG
                                                                                                                                                                                                                                                                                                                                                     ATTTGTTTCAGAGGAGATACATACGCTCTGTTCTTATAGCTTTCGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCGTGGGAAGAAGGCTGATATTTCGGAGGAG.....GCAGCAGAGAT 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTGGCAAAAGTGGGGGCGTGATACGGAGTTTGAAGCTGCACTGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heLeuLeuThrGlnHisArgArgGlnGlu...AlaIleAlaLeuArgPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAGGCACACTAGTGACGTGGAGAGTCTTGGCATTAATAGGAATCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCysValPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCGCTGCCTTCCTTGGCCTCTTTTTTATCCCTGAGTCTCCAAGAT
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207	ProProfleGlyAlaGluGlnSerPheHisLeuAlaLeuL	224
1335	TGAGCCGGAGGCAGGATGGTTTGATCTATTC	1371
224	ProGlyIleTyrLysProPheIleIleGlyValSerLeuMet	240
1372	TCTCTTC	1416
241	aValMetPheTyrAlaGluTh	257
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1467	GTAGTGCGGGAATCCAATCAGATGTTGCAGCCAGTGCTCTCG	1516
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341	AlaTrpLeuAlaValGlySerMetCysLeuPh	357
1660	AACTGTTCTATA	1703
357	eIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetS :::: :::   :::::            ::	374
274	NOT THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER	2
1754	CAGAGARATTTGCATCCCGAATCAGAACAAAAAGCCGTCCTCTTTTCTCTC	1803
391	NlaPheLeuValThrLysGluPheSerSerLe	407
1804	GGCATGCACTGGATATCAAACTTTGTGATCGGACTATACTTCTTAAGCGT	1853
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1854	TGTGACTAAATTCGGAATCAGCAGTGTCTACT	1885
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1886	TTTGCTGGAGTCTGCGTCCTTGCGGTCCTCTACATTGCAGGAAAC	1935
435	ValProGluThrLysGlyLysThrLeuGluGlnIle 446	
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Database sequences: 351203
Database length: 113238999
Search time (sec): 124.8300
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-928-692-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database:
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-O=/cgn2_1/USPTO_spoo1/US09516493/runat_13022002_125123_18457/app_query.fasta_1.894
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-DELDP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
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sequences: 351203
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Compugen Ltd.
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alignment_block:
US-09-516-493-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-727-034-2 - /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-03-840A-1 - /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-532-814-1 - /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-647-397-1 + /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-450-257-22 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8
LENGTH: 2592
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Patent No. 6303373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/154,078
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/138,237
PRIOR FILING DATE: 1999-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/591,025
CURRENT FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method of Measuring
TITLE OF INVENTION: Targeting of GLUT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 25
TYPE: DNA
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                                                                                                                                                                                                                                                                                               634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 CCAGCT...CCATCCCTCCAGGCACCCTCACCACCCTCT......
                                                                                                                                                                                                              684 CAGCCTCATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCC
                                                                                                                                                                                                                                                                                                                                  72 GlyArgLysLeuSerLeuLeuCysSerValProPheValAlaGly..
                                                                                                                                                                                                                                                                                                                                                                                                                  59 laGly......GlyValLeuGlyGlyTrpLeuValAspArgAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
ySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuA 152
                                                                          ProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGl 135
                                                                                                                         TTGGACGATTCCTCATTGGCGCCTACTCAGGGCTGACATCAGGGCTGGTG
                                                                                                                                                                 lyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuValAla
                                                                                                                                                                                                                                                   .....PheAlaValIleThrAlaAlaGlnAspValTrpMetLeuLeuG
                                                                                                                                                                                                                                                                                             GGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGG
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Lodish, Harvey F.
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alignment_block:
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                                                                                                                                                                US-09-516-493-7 x US-08-928-692-9
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                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                              585 TTTATCACAACTTTGGGGCCACTTCAATTCGGATATCATTTGGTATTACA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS: No form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 49.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1744 GACCAGATCTCGGCTGCCTTC 1764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 12-SEPT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 400
CITY: New York
CTATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 GluGlnIleThrAlaHisPhe 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
                                                                               8 PheAlaAlaAlaLeuGlyProLeuSerPheGlyPheAlaLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10174
CGGAGCTTGGTCTATGCTGGAGGCTTCAATACATCGGCTGACAATATATT 684
                              .GlyTyrSerSerProAlaIleProSerLeuGlnArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....PheThrLeuPheCysValProGluThrLysGlyLysThrLeu 443
                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                             H: 3000 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Application US/08928692 5958727
                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yaver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEPT-1997
                                                                                                                                                                                                                449.50
1.572
56.299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....GTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deborah S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                             9:
                                                                                                                                                                                                  Length: 508
Gaps: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4944.200-US
                                                                                                                                to: 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5958727th America, Inc
                                 33
                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1693
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34 685	AlaAlaProProAlaProArgLeuAspAspAla :::                         ATGATAGGCTGAGCTCAATGCCCCCCAGGCCGTGATAACTTGCGAGCGGA	44 734
	AlaSer	47
735	AGCATCCATTCGACAACAACACGGGGTCTCCCGCAATGCATACCTATG	784
48	TrpPheGlyAlaValThrLeuGlyAlaA	58
785	AATTCGGCCTGGTC.TCCTCTATATACACCCTTGGGGGCT	833
83.4 58	yValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLys ::::   :::    :::	74
7	.euSerLeuLeuCysSerValProPheValAlaGlyPheAlaValIl	<u> </u>
884	AGCGACCACCATCTTCTTCATCCTAGGCCCTATAGCAGA	933
91	hrAlaAlaGlnAspValTrpMetLeuGeuGlyGlyArgLeuLeuThrG	108
934	ATTTGCGCCCAGTATACCCGTATTGAGTATGGGTAGGCTTTTATCTG	983
108 984	rLeuValAlaProValTyrIleSerGlu :::   :::   :::	124 1033
125 1034	IleAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGlnLeuMe 	141 1083
141	IValValGlyTleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu.	157
1084	ACTAATGTCGGTATTCTGTTGACACAGTCCCTTGGTTACTTCTTGAGTA	1133
158 1134	roPro	169. 1180
7	LeuMetLeuLeuMetCvsPheMetProGluThrProArgPheLe	100 G
80 -	GCCTTGAGCTTCTGGGCCTCTTCTTAGTCCCAGAAAGCCCCATCTGGCT	N
186	ThrGlnHisArgArgGlnGluAlaIleAlaLeuArgPheLeuT	202
1231	GCAGATCACCAGAAAGGGAATGTGGCTAGACAGGTGCTACAACGTATAC	1280
202	GCACCCACACCTTCAACCACAACATCTTCAACAACAACATCTT	209
		(
210 1331	ProlleGlyAlaGluGlnSerPheHisLeuAlaLe	223 1368
223	gGlnPro	227
1369	CTATCACCCCATCTGGAAATATGCCACCCAAGCAACCTCCGGTTACCA	1418
Ñ	Gly11eTyrLysProPheI1eI1eGly	236
	CGAGCTATTACTGATTCTTTTTACCGCCCTGCCATCATTGCAGTG	1468
237 1469	ValSerLeumetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPh    ::::::   :::       ::::::::::::::::	253 1518
	ThrIlePheGluGluAlaLysPheLysAspSerSerLeuA	
1519	TACAGCGTTTCCCTCTTACAGACCATCCTTCCCACCACTGCAGCCC	1568

1569 287 1619 301 1669 318 318 318 31719 351 1719 351 1744 177 1785 385 1785 386 1785 386 1785 386 1785 386 1785 386 1785 387 1885 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 1785 1885 18	۵	<b>a</b>													
	lignment_scores: Quality: 425.00 Length: 47 Ratio: 1.471 Gaps: 1 Percent Similarity: 60.842 Percent Identity: 29.47	CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1 LENGTH: 4411529 TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv -09-103-840A-1	q_documentation_block: Sequence 1, Application US/09103840A Patent No. 629428 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN ELLE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A	eq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840	434 CysValProGluThrLysGlyLys 	417 heTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPhe 4 ::   ::::::::::::::::::::::::::::::::	401 rLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAlaP 417 ::::	385 AlaThrGlyILeCysValLeuThrAsnTrpLeuMetAlaPheLeuValTh 401     :: ::::: :::      :: ::   ::   :: 835 GCACAGAGCTGGGCGCTGGGAGCGAACTGGATTGCCACGTTCATCGTGGC 188	68 leProTrpLeuLeuMetSerGluIlePheProLeuHisValLysGlyVal 3 ::   ::::      :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::   :::   :::   :::   :::   ::	351 IGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProI 368	335 ValSerAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuAlaVa :::      736ATAGCAGT	euThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerAlaPro 334	rGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPheLysL 318     ::::::     ::::     :::::     :::::    ::::::	287 LeuIleMetAspArgAlaGlyArgArgLeuLeuLeuValLeuSe 301 :::    :::	569 TGTCGGTGATCATCTCGGCTATCAATCTTGTAATCACTCTGGCCTGCTCA 161

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67 uValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProP 8   ::::::	4 71745 6 71750
97 ValTrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyVa 1	13 71755 30 71760
130 alargGlyLeuLeuGlySerCysValGlnLeuMetValValValGlyIle 1 [	46 71765 59 71770
159 gTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuM 1 :::	76 71775 92 71780
193 GlnGluAlaIleAlaLeuArgPheLeuTrpGlySerGluGlnGlyTr 2 :::	208 3717837 225 717887
roGly	232 8717937 246
938GCCACGCTGTTCGTCATCGCGCTTCCTCGTCCAGATCAC 3  6 rGlyValAsnAlaValMetPheTyrAlaGluThrIlePheGluGluAlaL 2  1	7 6 7

	SOFTWARE:
	COMPUTER: IBM COM
	ZIP: 02110 COMPUTER READ
	STATE: COUNTRY
	STREET: 225 Franklin Street
	CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richard
	VENTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
	GENERAL IN APPLICAN' APPLICAN'
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	<pre>seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-031-392-1</pre>
	442 rLeuGluGlnIleThrAlaHisPhe 450       :::
442 3718515	426 PheSerValLeuPheThrLeuPheCysValProGluThrLysGlyLysTh ::: :::::              ::: 3718466GTCGCGTTCGTGGTCGTGTACCGCTTTGCGCCGGAGACCAAGGGCCGCAA
3718465	416GTGTGCTCGGCGGCGCAGGCGTTTTCGCGGTTCTCGCAACGTTCGCC
425	oromore ( avaladhemrn.eualaseraladheevs I
409 3718415	393 nTrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetG :         ::::::           :::::::: 3718366GACACTGACGGCCAACGCGATCGTTGCCGCCTTCTCGCTCACCATGCTGC
393 3718365	377 PheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAs          ::::::::::::::::::::::::::::
376 3718318	360 lyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGluIle
360 3718268	343 rValGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaG ::::      ::: :::::::               3718222CACGGGGCTGCTGCTTTGGGGTTCGCCGGCGTGCTGCTGTTCATCATCG
343 3718221	327 SerHisValAlaIleSerAlaProValSerAlaGlnProValAspAlaSe     :::        :::    :::: 3718181GCCGTGCTGATCACCGTATTCGCCAACGACTCCGATGGTGG
3718180	3718179AT
326	310 erAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAsnSer
310 3718178	293 yArgArgLeuLeuValLeuSerGlyValValMetValPheSerThrS
293 3718131	280 LeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGl ::::::      :::    3718082GCCGGCTTGGCGGGGGTGTGTCCTGCTTTCTGGTCGATCGGCTGGG
279 3718081	263 ysPheLysAspSerSerLeuAlaSerValValValGlyValIIeGlnVal     ::::: ::::::::::::::::::::::::::::

147 719	133 LeuLeuGlySerCysValGInLeuMetValValValGlyfleLeu
132 669	116 euValAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGly
116	99 tLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerL     :::       :::    :::    ::: 570 GCTCATTGTGGGACGCTTCATCATGGGCATAGATGGAGGCGTCGCCCTCA
99 569	87 GlyPheAlaVallleThrAlaAlaGlnAspValTrpMe :::
86 519	LeuLeuLeuCysSerValProPheValAla        ::::: acacTTTGCTGGCCAATAATGGGTTTGCAATT
73 469	56 yAlaAlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyA
56 419	ValThrLeuGl :::::: ;aCTGTGTCCAT
39 372	29 roSerLeu
29 328	GTGAATGCCCCCCACCCCGTACATCA
19 278	LeuSerPheGlyPh :::   TCCTT
	2-1 f
	-
	alignment_scores: Quality: 378.50 Length: 491 Ratio: 1.418 Gaps: 13 Percent Similarity: 54.379 Percent Identity: 26.884
	FILING DATE: 26-FEB-1998  ATTORNEY/AGENT INFORMATION:  NAME: Meiklejohn, Ph.D., Anita L.  REGISTRATION NUMBER: 35,283  REFERENCE/DOCKET NUMBER: 07334/072001  TELECOMMUNICATION INFORMATION:  TELEPHONE: 617/542-8906  TELEX: 200154  INFORMATION FOR SEO ID NO: 1:  SEQUENCE CHARACTERISTICS:  LENGTH: 2343 base pairs  TYPE: nucleic acid  STRANDEDNESS: single TOPOLOGY: ilnear  MOLECULE TYPE: cDNA FEATURE:  NAME/KEY: Coding Sequence LOCATION: 731761  US-09-031-392-1

446	uPheThrLeuPheCvsValProGluThrLvsGlvLvsThrLeuGluGlnI	429
429 155(	ProTyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLe	413 1504
412 150	etAlaPheLeuValThrLysGluPheSerSerLeuMetGluValLeuArg	396 1454
	isvallysglyvalalat) ::: :::    crcagcggccggctgcct	379 1404
379 140:	ValGlyTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProLe	363 1354
362 135:	euAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAla :: ::   ::::: ::::::::::::::::::::::::	346 1304
346 130:	SerAlaProValSer::::::::::::::::::::::::::::::::::::	329 1254
329 125:	SLeuThrGlnGlyGlyProGlyAsnSe	313 1228
2 1	Val\	296 1217
296 121	LeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgL	279 1167
279 116	LysaspSerSerLeuAlaSerValValValGlyValIleGlnVa ::::::::	265 1117
264 111	alAsnAlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPhe :::      :::      :::       :::	248 1067
248 106	euMetAla        CCATGGC	231 1017
231 101	LeuAlaLeuLeuArgGlnProGlyIleTyrLy	221 967
220 966	AlaGluGlnSerPheHis:       :::  GCTGAGAGCCACGTGCAG <i>E</i>	206 917
206 916	nGluAlaIleAlaLeuArgPheLeuTrpGlySerGluG:          :::::::::::::::::::::::::	193 867
193 866	CysPheMetProGluThrProArgPheLeuLeuThrGlnHisArgArgGl	177 820
176 819	rpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuLeuMet :::	160 770
160 769	LeuAlaTyrLeuAlaGlyTrpValLeuGluTrpArgT	148 720

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alignment_block:
US-09-516-493-7 x US-09-299-549-1
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; LOCATION:
US-09-299-549-1
                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                      Align seg 1/1 to: US-09-299-549-1
                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
   Sequence 1, Application US/09299549
   Patent No. 6136547
   Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASESEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/ACENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/072002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-299-549-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                  238 CTCCTCGTGGCCTCCCTCGGGGCGCCTTCGGCTCC......TCCTT 278
19 eAlaLeuGlyTyrSer....
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1601 TCAGCCAGGCATTTTCCAAAAGG 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1551 CTACCTGTATTTTGTGCTGCCTGAGACCAAAAACAGAACCTATGCAGAAA 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                       3 ValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPheGlyPh 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 leThralaHisPheGluGlyArg 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 F
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                        378.50
1.418
54.379
                                                                                                                                                                                                                                    Length: 491
Gaps: 13
Percent Identity: 26.884
                                                                                                                                   from: 1 to: 2343
              .....SerProAlaIleP 29
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279 LeubheThrAlaValAlaAlaLeuILeMetAspArgAlaGlyArgArgL 296
165 LysAspSerSerLeul ::::::::::::::::::::::::::::::::::::
6 4
31 sProPheIleIl ::: 17 GCAGGTGGTCAC
2167 ATCCGCCTGGTGTCC
106 lnGlyTrpGluAspProProIle
93 nGluAlaIleAlaLeuArg 
20 (
60 rpLeuAla ::    70 ACCTGTTT
48LeuAlaTyrLeu
33 LeuLeuGlySerCysValGlnLeuMetValVa 
20
9 tLeuLeuGlyGlyArgLe
7 GlyPheAl :::    0 TCTGCTGC
rgLysLeuSer ::    ::: AGGTTCTTGGGAGGAAGCA
yAlaAlaAlaGlyGlyValL           :::: ATTCGCCATCGGTGGACTTG
0 ArgLeuAspAspAlaAlaAlaSerTrpPheGlyAlaValValThrLeu ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
9 roSerLeuGlnArgAlaAlaProPy 
9 CCTCTACGCTACAACCTGTCGGTGGTC

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-501-572-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1551 CTACCTGTATTTTGTGCTGCCTGAGACCAAAAACAGAACCTATGCAGAAA 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1504 ACCTAC...TGTTTCCTAGTCTTTGCTACAATTTGTATCACAGGTGCTAT
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ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grundeman, Dirk APPLICANT: Gorboulev, Valentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446
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                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 I S
CITY: Washington
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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o. 6063623
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                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koepsell, Hermann
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                                                                                                                             US/08/501,572
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alignment_block:
US-09-516-493-7 x US-08-501-572-6
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; MOLECULE TYPE:
US-08-501-572-6
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Percent Similarity:
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INFORMATION FOR SEQ ID NO:
                                                1121 AAACTGGCAAGAAATTGAACCCT........TCATTT...CTT
                                                                                                                                                   1071 AAATGGAAAATCTCTACCCGCCTCCCTTCAGCGCCTGAGACTTGAAGAGG
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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222 AlaLeuLeuArgGlnProGlyIleTyrLysProPheIleIleGlyVal..
                                                                                                                                                                                                                                                                                            189 GlnHisArgArgGlnGluAlaIleAlaLeu.........
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                                                                                                                                                                                                                                                                                                                                            TCTTGCTCTATTACTGGTGCATACCTGAGTCTCCCAGGTGGCTGATCTCC 1020
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                                                                                                luGlnGlyTrpGluAspProProIleGlyAlaGluGlnSerPheHisLeu
                                                                                                                                                                                      .....ArgPheLeuTrpGlySerG
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seq_documentation_block:
                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-040-444-6
                                                                                                                                                                                                         Sequence 6, Application US/09040444 Patent No. 6063766
                                                                                                                                                                            GENERAL INFORMATION:
           APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCTGTCTGGCCTCAGTTTTTATA.....CCTGGTGA 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTGGTTCACGAGCTCTGTGCTCTACCAGGGCCTCATCATGCACATGG
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: 1; MOLECULE TYPE: US-09-040-444-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-040-444-6 from: 1 to: 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-516-493-7 x US-09-040-444-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
            921
                                                   155
                                                                                          871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                       821 CAGAATTTGTTGGGGGGAGATATCGGAGAACAGTGGGGATTTTTTACCAA 870
                                                                                                                                                                                          123 erGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGln 139
                                                                                                                                                                                                                                     771 CCAAGGACTGGTCAGCAAAGCAGGCTGGTTAATAGGCTACATCCTGATTA 820
                                                                                                                                                                                                                                                                          106 uThrGlyLeuAlaCysGlyValAlaSerLeuValAlaProValTyrIleS 123
                                                                                                                                                                                                                                                                                                                             724
                                                                                                                                                                                                                                                                                                                                                                                             674 AGCTCTGCCTCAACTACAGTCCTCATAAATGCTGCAGCTGGAGTTCTC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 CTTTATTGGCTCTATGAGTATCGGCTACATAGCAGACAGGTTTGGCCGTA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 GCCAACTCCTGGATGTTGGACCTATTCCAGTCATCAGTGAATGTAGGATT 623
                                                                                                                                                                                                                                                                                                                                                                    90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 aAlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgL 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TCCTCACTGGAGGTGGTTGCAGTTCACAGTTGCTCTGCCCCAACTTCTTCT
                            lLeuGluTrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuM
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                                                                                                              LeuMetValValValGlyIleLeu...LeuAlaTyrLeuAlaGlyTrpVa 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: O'CONDOR, Steven PREGISTRATION NUMBER: 41,
                                                                           GTTGCCTATACAGTTGGGCTCCTGGTGCTAGCTGGGGTGGCTTACGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                 ATGGCCATTTCCCCCAACCTATACGTGGATGTTAATT...TTTCGCTTAAT
                                                                                                                                                                                                                                                                                                                                                    ValIleThrAlaAlaGlnAspValTrpMetLeuLeuGlyGlyArgLeuLe 106
                                                                                                                                                                                                                                                                                                                                                                                                                                  ysLeuSerLeuLeu...LeuCysSerValProPheValAlaGlyPheAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202)408-4000
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1.210
47.556
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429	rpLeuAlaSerAlaPheCvsIlePheSerValLeu	418
6	CATTGGTGGCATCACCGCCATTCCTGGTCTACCGCCTCACTAACAT	
	luValLeuArgProffvrG]vA]aPhe	409
σ	:::TCCTCAATGTGT	555
408	uPheSerSerLeuMet	392
1554	TGTACCCCACATTCATTAGGAATCTTGGCGTCCACATCTGT	512
392	<pre>rlePheProLeuHisValLysGlyValAlaThrGlylleCysValLeuT</pre>	375
1511		.465
375	lyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGl	359
1464	ACAATGGCTAAAAATTATTATCTCATGCTTGGGAAGA	426
358	ValGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPhelle	342
1425		425
342	Ser Ser HisValAlaile Ser AlaProValSerAlaGlnProValAspA	325
1424	GCCTGTCTGGCCTCAGTTTTTATA	390
325	rSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAs	309
1389	CCGTTACCCTTGGGCTGCATCAAATATGGTTGCAGGG	346
308	lyArgArgLeuLeuLeuValLeuSerGlyValValMetValPheSer	292
1345	ATGATCATCCTCATTATCGACCGCA	.321
292	alLeuPheThrAlaValAlaAlaLeuTleMetAspArgA	275
1320	TTCCCAGCTGCCTTC	303
275	uAlaLysPheLysAspSerSerLeuAlaSerValValValG!	259
1302		253
258	uSerGlyValAsnAlaValMetPheTyrAlaGluThrIle	244
10 4	AGCTCTGTGCTCTACCAGGGCCTCATCATGCACATGG	0
<u>.</u>	correct to Mot A leabhorless	نہ
1202	TACTATGATATTGATGTA	153
J		J t
221	TIGLY TIPGLUAS PROPROPROLIEG LYALAG LUGLUS EST PHENS LEU 	121
	ATGGAAAATCTCTACCCGCCTCCCTTCAGCGCCTGAGACTTGAAGAGG	<b>`</b>
0.5	ArgpheLeuTrpGlySerG	9
1070	AGAATAAGAATGCTGAAGCCATGAGAATCATTAAGCACATCGCAAAGAA	021
198		189
1020	GGTGCATACCTGAGTCTCCCAGGTGGCTGATCTCC	971
188	tLeuLeuLeuMetCysPheMetProGluThrProArgPheLeuLeuThr	172

AlaGlvGlvValLeuGlvGlvTrpLeuValAspArgA	28IleProSerLeuGlnArgAlaAlaProProAlaProArgLeuA	12 LeuGlyProLeuSerPheGlyPheAlaLeuGlyTyrSerSerProAla	Align seg 1/1 to: US-08-501-572-4 from: 1 to:	alignment_block: US-09-516-493-7 x US-08-501-572-4	alignment_scores: Quality: 245.00 Ratio: 1.061 Percent Similarity: 48.632 Percent Identity:	Grundeman, Dirk Gorboulev, Valentin NVENTION: Transport protein which NVENTION: DNA Sequences Encoding SEQUENCES: 6 ENCE ADDRESS: E: Finnegan, Henderson, Farabow, Gar 1300 I Street, N.W., Suite 700 Tashington D.C. USA 005-3315 EADABLE FORM: SEADABLE FORM: IBM PC compatible G SYSTEM: PC-DOS/MS-DOS TION NUMBER: US/08/501,572 ATE: CATION: 424 CATION DATA: CONTON INFORMATION: CONTON INFORMATION: CONTON INFORMATION: E: (202)408-4400 FOR SEQ ID NO: 4: HARACTERISTICS: 1882 base pairs UCLeic acid NESS: single Linear YPE: DNA (genomic)	seq_documentation_block: ; Sequence 4, Application US/08501572 ; Patent No. 6063623 ; CENERAL INFORMATION: ; APPLICANT: KOPOSEO!! Hermann	seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-501-572	1667 GAGGTCTGGTGCTTGCTTCCAGAAACTAAAGGGAAAGCTTTGCCTGAG
7 5	ProAlaProArgLeuA 42     :::::   GACGCCTGGAAAGTGG 485	yrSerSerProAla 27   :::::   :::  ACGACACTCCCGGCTC 435			ngth: 475 Gaps: 21  tity: 25.474	which Effects The onic Xenobiotics and\or Pharmaceuticals, oding It And Their Use.  Now, Garrett & Dunner 7000  ersion #1.30		1:US-08-501-572-4	

MOLECULE TYPE: DNA (genomic)	<u>×</u>	
TOPOLOGY: linear	•• •	
nucleic acid		
EQUENCE CHARACTERISTICS;	·· ··	
INFORMATION FOR SOCIED ID NO: 4:	; INF	
TELEPHONE: (202)408-44000 TELEPAX: (202)408-4400	٠. ٠.	
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CLASSIFICATION:		
APPLICATION NUMBER: US/09/040,444 FILING DATE: March 18. 1998	٠. ٠,	
URRENT APPLICATION DATA:		
Social		
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	٠. ٠.	
COMPUTER READABLE FORM:	;	
COUNTRY: USA ZIP: 20005-3315	•• ••	
STATE: D.C.	•••	
STREET: 1300 I Street, N.W., Suite 700		
Finnegan Henderson Farabow Carrott & Dunney I I	·· ··	
NUMBER OF SEQUENCES: 6		
AVENTION: Transport Of Cationic Xenobiotic		
WENTION: Transport protein Whi		
APPLICANT: Grundeman, Dirk		
	; GE	
A_VOCUMENTALION_DIOCK: Sequence 4, Application US/09040444 Patent No. 6063766	; Seq_u	
/cgn2_6,	eq	
437 uThrLysGlyLysThrLeuGluGln 445            585 GACCAAGGTTTTGCCTTAGC 1609	L	
427 SerValLeuPheThrLeuPheCysValProGl 437 :::      1538 GGGGTTTTGGGCCTGACTGCTGGGGCCATGACTCTTCTTCTCCCAGA 1584	1	
410 alLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePhe 426	<u>.</u>	
393 nTrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetGluV 410 : :::         :::       :::	F-4	
381 421	Ŀ	
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laGlyPheAlaValG		
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US-09-040-444-4

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alignment_block:
US-09-516-493-7 x US-09-040-444-4
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Percent Similarity:
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1062 CCAACCTGAGGAAGCACACCGTCATCCTGATGTATCTATGGTTCTCTTTGT 1111
                                                                                                              1015 TGCCTCAGAAAAGCGAAGTCCTTCGTTT...GCCGACCTGTTCCGCACTC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                              227 roGlyIleTyrLysProPheIleIleGlyValSerLeu...... 239
                                                                                                                                                                                                                          965 AACGGGAAGGTGCCTCCTGCTGACCTGAAGATGCTCTGCCTTGAGGAGGA 1014
                                                                                                                                                                                                                                                                              206 GlnGly......TrpGluAs 210
                                                                                                                                                                                                                                                                                                                                      915 AGAAGAGAACCACGCGAGCTGTCAGGATAATGGAGCAAATTGCACAGAAG 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                765 TGGCCTTCACAGTGGGGCTAGTGGGGCTTGCCGGGGTGGCCTATGCCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 leThrAla...AlaGlnAspValTrpMetLeuLeuGlyGlyArqLeuLeu 106 ::|||||| ||| ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 AlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 uSerLeuLeuCysSer...ValProPheValAlaGlyPheAlaValI 91
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                                                                                                                                              Quality:
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48.632
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Caps: 21
Percent Identity: 25.474
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ier	CORRE ADD STR CIT	
he and\or	atent No. 6063623  GENERAL INFORMATION: APPLICANT: Koepsell, Hermann APPLICANT: Grundeman, Dirk APPLICANT: Gorboulev, Valentin APPLICANT: Gorboulev, Valentin TITLE OF INVENTION: Transport protein which Effects T TITLE OF INVENTION: Transport Of Cationic Xenobiotics TITLE OF INVENTION: DNA Sequences Encoding It And The	
	eq_name: eq_docume Sequence	
	437 uThrLysGlyLysThrLeuGluGln 445	
437 1584	427 SerValLeu	
426 1537	410 alLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePhe	
410 1508	393 nTrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetGluV :::    :::    ::: 1471 GATCTTCACCCCCTTCATGGTGTTCAGGCTGATGGAAG	
393 1470	381 ValLysGlyValAlaThrGlyIleCysValLeuThrAs ::::::::::::::::::::::::::::::::::::	
380 1420	364 lyTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHis :::    :::::   :::::    1374 TGCTGCAGATGGTCTGCCTGGTGAACGCTGAGCTGTACCCTACATTC	
364 1373	347 aTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValG	
347 1323	331 IleSerAlaProValSerAlaGlnProValAspAlaSerValGlyLeuAl	
330 1300	314 laTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAla	
314 1276	297 uLeuValLeuSerGlyValValMetValPheSerThrSerAlaPheGlyA ::::::    :::::    1255 AATAGCGGCCTCGAATCTGGTG	
297 1254	281 PheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLe ::: :::             1214ATGATCCTGGTCACCATTGACCGCATTGGCCGGATCTACCC	
N	12 TC	
294 1211 280	249 INTERVALUEL	
A 1-4 A	40MetAlaPheGlnGlnLeuSerGlyValA ::: ::        12 GCTGTGCTGTACCAGGGTCTCATCATGCACGTGGGAGCCACAGGGGCCA  A0 CAlaValMot	

Pharmaceuticals,

4 euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAla 14
117 lalaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL 134 ::::     :::    :::::
101 LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa 117
92 hralaalaginaspValTrpMetLeu 100 ::   :::::
75 uSerLeuLeuCysSerValProPheValAlaGlyPheAlaValIleT 92
59 AlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLe 75
42 spAspAlaAlaSerTrpPheGlyAlaValValThrLeuGlyAlaAla 58
28IleProSerLeuGlnArgAlaAlaProProAlaProArgLeuA 42 ::: ::::::::::::::::::::::::::::::::
12 LeuGlyProLeuSerPheGlyPheAlaLeuGlyTyrSerSerProAla. 27
Align seg 1/1 to: US-08-501-572-5 from: 1 to: 1885
alignment_block: US-09-516-493-7 x US-08-501-572-5
alignment_scores: Quality: 220.50 Length: 467 Ratio: 0.946 Gaps: 15 Percent Similarity: 49.893 Percent Identity: 23.555
TOPOLOGY: linear MOLECULE TYPE: DNA (9 S-08-501-572-5
TYPE: nucleic acid STRANDEDNESS: singl
SEQUENCE CHARACTERIS LENGTH: 1885 base
TELEPHONE: (202)408-4000 TELEFAX: (202)408-4400 INFORMATION FOR SEC ID NO: 5.
REFERENCE/DOCKET NUMBER: 02481.1453-00000  TELECOMMUNICATION INFORMATION:
CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/501,572 FILING DATE.
COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patent
ZIP: 20005-3315 COMPUTER READABLE FOR MEDIUM TYPE: Flor
STATE: D.

132	laPheCysIlePheSerValLeuPheThrL 	417 1540
117 1539	erSerLeuMetGluValLeuArgProTy	400 1521
100 1520	ValalaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeuVa 4    ::::::::   :::    :::   GTGTGTTCCTCCCTGTGTGACATAGGTGGGATAATCACCCCCTTCATAGT 1	384 1471
383 1470	TCAGAGTGATG	371 1421
371 1420	lyTrpGlyProIleProTrpL :: CAATACAAATGATCTGCC	354 1374
35 <b>4</b> 1373	SPAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMe 	338 1324
337 1323	yGlyPrOGlyAsnSerSerHisValAlaIleSerAlaProValSerAla     ::::::: 	1309
1308		1308
321	${\tt MetValPheSerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnG}$	304
304 1307	IleMetAspArgAlaGlyArgArgLeuLeuValLeuSerGlyValVa :::      :::      accarreaccecgregeccccarcraccccargecgregoccaantregre	288 1258
287 1257	erValValClyVallleGlnValLeuPheThrAlaValAlaAlaLeu ::: :::::::::::::::::::::::::::::::::	271 1208
271 1207	rAlaGluThrIlePheGluGluAlaLysPheLysAspSerSerLeuAlaS :::	254 1158
254 1157	lyValAsnAlaValMetPheTy :::::::   :::: TCACGGACTCTGTGCTCTATCA	238 1120
237 1119	euAlaLeuLeuArgGlnProGlyIleTyrLysProPheIleIleGlyVal	221 1076
221 1075	GCTTTCCCTCGAAGAGGATGTCACCGAAAAGCTGAGCCCTTCATTTG	N C
0	ACATCGCTCAAAGAATGGGAAGTTGCCTCCTGCTGATTTAAAGA	
207	erGluGlnGly	200
199 978	roArgPheLeuLeuThrGlnHisArgArgGlnGluAlaIleAlaLeuArg 	183 929
183 928	SValProProSerLeuMetLeuLeuMetCysPheMetProGluThrP:::         :::       :::      :::	166 879
166 878	TyrLeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCy         	150 829
828	TGGCGATCATGTACCAGATGGCCTTCACGGTGGGGCTGGTGGCGCT	7

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Search completed: February 13, 2002, 20:05:31 Job time: 18158 sec
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                                                                                                                                                                                                                                                                                                                      ; ORGANISM:
US-08-948-176-20
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-8926-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEPHONE: 302-973-0164
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                  Ouery Match 5.2%; Score 54; DB 2; Length 13; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 54; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,176

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/631,264

FILING DATE: DECEMBER 20, 1990

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNNE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: HITZ, WILLIAM D.

APPLICANT: YADAV, NARRNDRA S.

TITLE OF INVENTION: ACYL-ACP THIOESTERASES GENES
TITLE OF INVENTION: AND THEIR USE IN ALTERING PLANT
TITLE OF INVENTION: OIL COMPOSITION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                          STREET: 1007 MARI
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                         Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                               Length 1378;
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                                                                                                                                                                                                  Gaps
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; TOPOLOGY: US-08-818-112-14
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                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-MAR-199
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELLEFAX: (,, TELLEFAX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                           TYPE:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                 TELEPHONE:
                                                                                                                                                                                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                             98104-7092
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                                                        1058 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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              linear
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                                                                                                                 (206) 622-4900
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                                                                                                                                                                                                                        13-MAR-1997
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                          single
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Pred. No. 5.8e-13;
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US-08-948-176-20

: Sequence 20, Application US/08948176

: Patent No. 5945585
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Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                         MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Bras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MORRISSEY, Bruce W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hitz, William D.
APPLICANT: Yadav, Narendra S.
TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                 71 TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAG 124
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Morrissey, Bruce W
REGISTRATION NUMBER: 30,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1007 Marl
                                                                                                                 1 tggcggccgctctagaactagtggatcccccgggctgcaggaattcggcacgag
                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                               54;
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nucleic acid
DEDNESS: single
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Similarity 100.0%; Pred. No. 5.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), Application US/08075533
5530186
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (302) 892-7949
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                                                                                                                                                                                                                                                              Brassica napus
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                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         (302) 992-4927
                                                                                                                                                                                                                                                                                           DNA (genomic)
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    du Pont de Nemours and Company

                                                                                                                                                                              5.2%; Score 54; 100.0%; Pred. No.
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                                                                                                                                                             Mismatches
                                                                                                                                                                               DB 1; L. 5.1e-13;
                                                                                                                                                                                           Length 1378;
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US-08-341-568-1
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US-08-818-112-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                            TITLE OF INVENTION: Mannanase
TITLE OF INVENTION: methods for
TITLE OF INVENTION: pulps
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
                                                                                                                               CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                        APPLICANT:
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OPERATING SYSTEM:
                                                                    STATE:
                                                                                                 STREET:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
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STATE: Washington
                                   ZIP: 22040-0747
                                                COUNTRY:
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VA
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                                                                                                E: Birch, Stewart, PO Box 747
                                                                                                                                                                                                           Marjatta, Ranua
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Saloheimo, Anu
                                                                                                                                                                                                                                                       Viikari, Liisa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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100.0%;
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                                                                                                                Kolasch and Birch
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                                                                                                                                                                       enzymes, genes coding for them, or isolating the genes, and methods for bleaching light
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                     APPLICANT: Saloheimo, Anua APPLICANT: Marjatta, Ranua TITLE OF INVENTION: Methods TITLE OF INVENTION: 1ignoce
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LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: "11 ORGANISM: "11 QM9414
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TEX: 248345
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                                                                                                                                                                                                                                         STREET: PO Box 747
CITY: Falls Church
                                                                          APPLICATION NUMBER: US/0 FILING DATE: 13-AUG-1997
                                                             CLASSIFICATION:
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                            Birch,
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                                                                                                                                                                                                                                                                                                            lignocellulosic pulps
                                                                                                                                                                                                                                                                                                                                     Mannanase enzymes, genes coding methods for isolating the genes,
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                                                                                        US/08/911,020
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                                                                                                                        Version #1.30
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. 5.8e-13;
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                                                                                                                                                                                                                                                                                                                                       and methods for bleaching
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                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/341,568
APPLICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 28,977
                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                           REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: lignocellulosic pulps
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ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
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CITY: Falls Church
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                                                                                                LENGTH:
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                                                                               nucleic acid
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                                                                                           289 base pairs
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PO Box 747
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Siika-aho, Matti
Viikari, Liisa
Penttila, Merja
Saloheimo, Anu
Marjatta, Ranua
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Trichoderma reesei
                                              linear
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Pred. No.
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. 6.3e-13;
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US-08-818-112-101/c
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                                                                                                                   RESULT
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                           Sequence 101, Application US/08818112 Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, SLEVELL.

APPLICANT: Dillon, Davin C.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Micham, Jennifer L.

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APPLIC
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H: 375 base pairs nucleic acid DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                               Score 54;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                               DB 3; Lo
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                                                                                                                                                                                                                                                                                                                                                                       Length 375;
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APPLICANT: APPLICANT:

Reed, Steven G. Skeiky, Yasir A.W.

COMPUTER READABLE FORM:

COUNTRY:

OPERATING SYSTEM: MEDIUM TYPE:

Apple Macintosh Diskette,

3.50 inch, 1.0

MB

Macintosh 7.0

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                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                    Sequence
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Best Local
                                                                                                                                                                                                                                                                                                                         GENERAL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                   APPLICANT: Sullivan, Robert
APPLICANT: Brub, Bruno
APPLICANT: Lgar, Christine
APPLICANT: Gaudreault, Christian
TITLE OF INVENTION: Acrosomal Sperm Protein And
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN 07/968,971
FILING DATE: 30 October, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1601 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 29 OC
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               SOFTWARE:
                                                                                                          COUNTRY:
                                                                                                                             STATE:
                                                                                                                                                           STREET:
                                                                                                                                                                          ADDRESSEE:
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NO. 5989549
                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                           E: QC
TRY: Canada
H3A 2Y3
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APPLICATION DATA
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(916) 753-1510
R SEQ ID NO: 6:
             SYSTEM: Windows FastSEQ for Windows Version 2.0b
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500 - 1981 McGill College
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 56; DB 1; 100.0%; Pred. No. 8.1e-1
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US-08-341-568-3
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                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: renucation, Anu APPLICANT: Saloheimo, Anu APPLICANT: Marjatta, Ranua APPLICANT: Marjatta, Ranua Enzymes, genes coding for them, TITLE OF INVENTION: methods for isolating the genes, and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 26,674
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514,845-7126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Kevin P
REGISTRATION NUMBER: 26,
                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 912 base pairs
                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 22-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                    STREET: PO Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
                               TELEPHONE:
                                                                    REFERENCE/DOCKET NUMBER:
                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/090,567 FILING DATE:
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PO Box 747
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100.0%; Pred. No. 2.2e-13;
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                                                                                                                                                                                                                                Sequence 10, Application US/07968971A Patent No. 5455167
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Best Local Similarity
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                                          GENERAL INFORMATION:
APPLICANT: Toni A. Voelker
APPLICANT: Huw Maelor Davies
TITLE OF INVENTION: Medium-CI
TITLE OF INVENTION: In Plant:
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08905445 Patent No. 5864015
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APPLICANT: Pfreun
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             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-MAY-PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                16 TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAGCTG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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Pred. No.
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Best Local :
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Davis
CA
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; MOLECULE TYPE: US-07-968-971A-10
                                                                                                                            Sequence 6, Application US/08424406 Patent No. 5667997 GENERAL INFORMATION:
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APPLICATION NUMBER: PCT/US'
FILING DATE: 21-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
NAME: Tizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (916) 753-15
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/782
FILING DATE: 24-OCT-1991
PRIOR APPLICATION UMBER: 07/824
APPLICATION UMBER: 07/824
FILING DATE: 22-JAN-1992
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                          APPLICANT: Voelker, Toni Aloi
APPLICANT: Davies, Huw Maelor
                                                            TITLE OF INVENTION:
                                                  NUMBER OF SEQUENCES:
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SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
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CITY: L
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                                                                                                                                                                                                                                     APPLICATION NUMBER:
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56; Conservative
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US-08-680-395-4
                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE,DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Hwang, Soo-in
APPLICANT: Godfrey, Tony
APPLICANT: Kowbel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40
MOLECULE TYPE:
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                   LENGTH:
TYPE: n
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
ZIP: 941
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0: FILING DATE: 15-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcac
CITY: San Francisco
STATE: California
                   TOPOLOGY: 111
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US-09-100-391-5

US-09-100-391-11

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US-08-758-621-7

US-08-758-621-7

US-08-0107-858-7

US-09-018-584A-35

US-09-018-584A-35

US-08-417-114-1

US-08-231-565A-1

US-09-207-961-1

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US-09-207-981-1

US-08-8192-770-4

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US-08-668-128B-7
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Best Local S
Matches 58
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7,
                                                                                                                                                                                                    TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,98
FILING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/644,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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LOCATION: 1..2605
OTHER INFORMATION:
OTHER INFORMATION:
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58;
                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
ZIP: 1
  16
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                NAME: Hanson, No. 5840568man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Third A CITY: New York City
TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
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805 Third Avenue
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ilarity 100.0%;
Conservative
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2) 838-3884
2 NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUNE-1996
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transcript"
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                                                   Score 57; DB 2; L; Pred. No. 3.1e-14; 0; Mismatches 0;
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07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                         11-APR-1997;
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Feng Kyaw Bednarik / н, Lafleur DW, Ferrie AM, Brewer LA, Soppet DR, C IA, Carter KC, Duan R, Ebner R, Fischer CL, Florence KA, Greene JJ, Li Y, Moore PA, Ni J, Olsen HS, Soppet DR, Young PE, Yu GL, Zeng Z Zeng Z; JM, Hu JS; S, Rosen CA; Endress GA;

P-PSDB; 1998-506364/43. AAW74910

New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 423-424; 721pp; English.

This sequence represents a nucleic acid molecule designated Gene 183 from the human cDNA clone HTOAF35 (deposited as clone ATCC 97904 and ATCC 209050) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathologonditions can be diagnosed by determining the amount of polypeptides in a sample or by determining the presence of polypeptides. Also, pathological presence of the new mutations in of

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes one of 32 novel human secreted polypeptides the nucleic acid molecules and polypeptides they encode may be used in the prevention diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
  01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 743; 890pp; English
                                          AAF97920
                                                                                AAF97920 standard; cDNA; 1149
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                                                                                                                                                                                    987
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1071 BP; 256 A; 310 C; 321 G; 180 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                          their expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing,
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protein coordinate data; infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein; immunomodulatory; antisclerotic;
ological; antiinflammatory; anti-HIV; cytostatic; cardiant;
ar; anti-anglogenic; ophthalmological; neuroprotectant;
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acids encoding 32 human secreted polypeptides, useful for ing, diagnosing and/or treating e.g. cancers, Parkinson's and diabetic retinopathy -
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                                                                                                                                                                                                                                                                Conservative
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e PA, Olsen
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Pred. No.
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sen CA, Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy, neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of
                                                                                                                                                                                                                                                              Sequence 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -  \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{2} \frac{1}{
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protein coordinate data; infection; ss.
AAV59693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The nucleic acid molecules and polypeptides they encode may the prevention, diagnosis and treatment of diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes one of 32 novel human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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nootropic; anticonvulsant; antialzheimers; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafleur DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2000;
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nes 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 744;
standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US26013
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antiinflammatory;
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e PA, Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 A; 334 C;
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ammatory; anti-HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:
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cytostatic; cardiant;
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be used in
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Human secreted protein gene 183 clone HTOAF35

19-JAN-1999

(first entry)

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07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 11-APR-1997;

> 97US-0040162. 97US-0040163. 97US-0040333.

97US-0040334 97US-0040336 97US-0040626 97US-0043311 97US-0043312 97US-0043313 97US-0043568 97US-0043568 97US-0043576 97US-0043576 97US-0043578 97US-0043578

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RESULT 1
AAF97918
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                             from the human cDNA clone HTOAF35 (deposited as clone ATCC 97904 and ATCC 209050) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in sea AAV5751 for described uses.
                                       AAF97918 standard; cDNA; 1071
                                                                                                                                                          1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feng P,
Kyaw H,
AAF97918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 540-541; 721pp; English.
                                                                                                                                                                        (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW75023.
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                                                                                                                                                   sequence represents a nucleic acid molecule designated Gene
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                                                                                                                                                                                                                                                                   Similarity
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Ferrie AM, Fischer (
Lafleur DW, Li Y, N
, Shi Y, Soppet DR,
                                                                                                                                                                                                                                                                                                                                                          2025 BP;
                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                 5.8%;
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                                                                                                                                                                                                                                                                                                                                                          527 C;
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                                                                                                                                                                                                                                                                 Score 60;
Pred. No.
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                                                                                                                                                                                                                                              Mismatches
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Florence KA, Greene JM, Hu JS;
re PA, Ni J, Olsen HS, Rosen CA;
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J. 3.6e-12;
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, neurological disorders (e.g., Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein encoding cDNA of the invention.
                                                     24-APR-1998;
                                                                                                                             04 - NOV - 1999
                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                          animal feed;
                                                                                                                                                                                                                                                         Inositol 1,3,4-triphosphate 5/6-kinase;
myo-inositol 1,2,3,4,5,6-hexaphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
               (DUPO ) DU PONT
                                                                                                                                                                   W09955879-A1
                                                                                                                                                                                                                                                                                                                 Rice inositol 1,3,4-triphosphate 5/6-kinase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ48807 standard; cDNA; 1574 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode AAB87414-AAB87454 represent human secreted protein fragments. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                          22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1086 BP; 260 A; 316 C; 326 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing, treating or ameliorating a disorder, e.g. Alzheimer's {\tt Parkinson's} diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or ameliorating medical conditions, e.g., by protein or gene Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                            SS
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                                                     98US-0082960
                                                                                        99WO-US08790
               DE NEMOURS & CO E
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; I
4.1e-12;
                                                                                                                                                                                                                                                         phytic acid;
biosynthetic
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                                                                                                                                                                                                                                                         genetic mapping enzyme; phytate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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21;

Length 1574;

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species, as well as for physical mapping. Decreased amounts of phytate and increased amounts of available phosphate in animal feeds such as correct would lead to improved feed efficiency. The proteins of the present invention lead to a better understanding of the phytic acid biosynthesis packagy, allowing it to be exploited for commercial uses, e.g. in animal
                                                                                                                                                  or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of 1,3,4-triphosphate 5/6 kinase found in those cells. In addition, it may be desirable to eliminate expression of ITK genes for certain applications. The polynucleotides also serve as a source of probes and primers, which are useful for genetic mapping, as markers for traits linked to those genes, and to isolate homologous sequences from other
Sequence
                                                                                                                                                                                                                                                                                                               protein of the invention. ITK is a phytic acid (Myo-inositol 1,2,3,4,5,6-hexaphosphate) biosynthetic enzyme. The ITK enzymes of the invention may be prepared recombinantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides of the invention may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                 create transgenic plants in which the ITK levels are present at higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence encodes an inositol 1,3,4-triphosphate 5/6-kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phytic acid biosynthetic
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1574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plants
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B₽;
370 A; 551 C;
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382 G;
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271
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                                                                                                                                                                                                                                                                                                                                                                                                                  (ITK)
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AAV59809
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Best Local Similarity
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 02-OCT-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                                                                                          osteoporosis; artnriti
endocrine; metabolism;
                                                                                                                                                                                                                          cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymoosteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaem; developmental abnormality; foetal deficiency; blood; allergy; renal; ds
                                                                                                                                                                                                                                                               immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-1998;
                                                                                                                                           W09839448-A2
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein gene 183 clone HTOAF35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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97US-0061060.
97US-0038621.
97US-0040161.
                                                                       98WO-US04493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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100.0%;
                                                                                                                                                                                                             regulation;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                           lung; thyroiditi
n; malabsorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
3.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                  osteoclast; thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                  leukaemia;
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RESULT
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Best Local
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                   Claim 1; Page 744; 890pp; English
                                                                     Nucleic acids encoding 32 human secreted preventing, diagnosing and/or treating edisease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular; anti-angiogenic; ophthalmological; neuroprotectant;
nootropic; anticonvulsant; antialzheimers; antiparkinsonian;
antimicrobial; vulnerary; vaccine; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed (see AAV34154 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-2000; 2000WO-US26013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200121658-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein coordinate data; infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF97921 standard; cDNA; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 70 novel genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological
                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF97921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunogle cortion (e.g. AAV34145) for increasing the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the fuseon the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability of the stability 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein as compared to the human protein only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                2001-235311/24
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                                                                                                                                                                                                                                                                                         Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted protein; immunomodulatory; antisclerotic;
ological; antiinflammatory; anti-HIV; cytostatic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 5.8%; l Similarity 100.0%; 60; Conservative
                                                                                                                                                                                                                                                              D₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       737
                                                                                                                                                                                                                                     Wei P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                99US-0155709.
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                                                                                                                                                                                                                                                                                       Birse CE, Ebner R,
                                                                                                                                                                                                                       Florence
                                                                                                                                                                                                                                                           Olsen HS,
                                                                                                                                                                                                                                     KΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 T; 13 other;
                                                                                             ed polypeptides, useful for e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                    Fiscella M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
4.5e-12;
                                                                                                                                                                                                                                                           Ruben
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                                                                                                                                                                                                                                                      Komatsoulis GA;
SA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the fused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes one of 32 novel human secreted polypeptides. The nucleic acid molecules and polypeptides they encode may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HTV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders
                                                                                                                                                                           03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                               Soppet
                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                          31-AUG-2000; 2000WO-US24008
                                                                                                                                                                                                                                                                                          WO200118022-A1
                                                                                                                                                                                                                                                                                                                                                     binding partner identification; ss
                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF91929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1086 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of
                                                                                                                                                                                                                                                          15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                       endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF91929 standard; cDNA; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                       culture; chemotaxis; food additive;
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                                                                                            DR,
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                                                                                                           Baker KP,
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                                                                           Young PE,
Shi Y, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                           99US-0152315.
99US-0152317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-encoding gene 51 cDNA clone HAPQT56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and activity.
                                                                                                         Birse CE,
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                                                                        se CE, Fiscella M,
Ebner R, Duan DR,
i Y, Florence "
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on; wound healing; vulnerary;
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Pred. No.
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4.1e-12;
                                                                                                           Komatsoulis GA,
                                                                                            Olsen HS,
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Nucleic acid molecules

encoding human secreted proteins, used

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P-PSDB;

2001-203081/20

AAB87413

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XX AV3
XX Huma
XW Huma
XW Infil
XW cogn
XW endc
XX End
XX Homc
XX Homc
XX Homc
XX PR 07-PP
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Best Local Similarity 100.0%;
Matches 62; Conservative
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||
2276 cc 2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymu osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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97US-0043568

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No.
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7.1e-13;
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97US-0056889
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(HUMA-) HUMAN GENOME SCI INC

Feng Kyaw Bednarik n SM, Lafleur I ₽₽, DP, Brewer LA, Ferrie AM, Fis e AM, rii aur DW, Li Y, Mc a Y, Soppet DR, or LA, Carter KC, Duan R, Ebner R, Fischer CL, Graves KA, Greene JR, Li Y, Moore PA, Ni J, Olsen HS, Soppet DR, Young PE, Yu GL, Zeng Z; Endress Hu JS; Rosen C GA;

WPI; 1998-609887/51. P-PSDB; AAW75173.

New isolated $\ensuremath{\text{ew}}$ isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological

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RESULT
AAC59424
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Best Local S
Matches 62
marrow,
(b) imm
                                  The invention relates to the isolation of genes AAC59392-C59439 encoce 48 human secreted proteins AAB33963-B34006. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes a proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overlan cancer, e.g. breast and overlan cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                        and ovarian cancer, and other cancers of the adrenal gland, bone, bone
                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC59424 standard; cDNA; 1547
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62; Conser
breast, gastrointestinal une disorders e.g. Addiso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1037
                                                                                                                                                                                              Page 347-348; 410pp; English
                                                                                                                                                                                                                             s
                                                                                                                                                                                                                            treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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99US-0169623.
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                                                                                                                                                                                                                                                                                                                                                      SCI INC
                                                                                                                                                                                                                                                                                                                            Komatsoulis
                                                                                                                                                                                                                            cancers
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tract, live
n's disease,
                                                                                                                                                                                                                                                                                                                         G;
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           liver,
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8.2e-13;
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          lung,
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             or urogenital;
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                                                                                                                                                                 encoding
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Best Local
                                                                                                                                                                                                                                                                                           Zea
                                                                                                                                                                                                                                                                                                           Starch-associated transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1483
                                                                                   corresponding
                                                                                           DNA encoding
                                                                                                              P-PSDB;
                                                                                                                                      Emmermann M,
                                                                                                                                                       (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
                                                                                                                                                                       19-DEC-1996;
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                                                                                                                                                                                                                         DE19653176-A1
                                                                                                                                                                                                                                                                                                                                    Maize starch-associated
                                                                                                                                                                                                                                                                                                                                                     07-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                         25-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                      AAV44318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1547 BP; 410 A; 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                           mays
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                                                                                                                     1998-349465/31
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                                                                                                             AAW64231
                                                                                                                                                                                                                                                                                                                                                                                                                                 1544
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                                                                                  maize starch-associated protein in potatoes g protein, vectors, transgenic plants, antibo
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                      Kossmann
                                                                                                                                                                       96DE-1053176
                                                                                                                                                                                        96DE-1053176
                                                                                                                                                                                                                                                                 Location/Qualifiers 33..1946
                                                                                                                                                                                                                                                /product= "starch-associated
                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                           protein; maize; starch grain; soluble;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune thyroiditis,
                                                                                                                                                                                                                                          "no start codon
                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           С;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                    CDNA
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                   antibody, starch,
                                                                                           and
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Sequence 2307 BP; 693

Α;

436 C;

555 G;

623

T; 0 other

Such a protein

equence encodes a novel maize starch-associated protein that both bound to starch grains and in soluble form in plant ce protein can be used to produce transgenic plants or plant co

cells

which are

capable

of synthesising modified

starch.

Claim

1; Page 43-46; 55pp; German.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
cancer antigens have cyrusucurus therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with happropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                           the proteins are collectively known as colon cancer antigens cancer antigens have cytostatic activity and can be used in g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                   cancer-associated nucleic acid molecules (N) and proteins (P),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignancies, diseases of testes, lung or thymus, digestive/endocrin disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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1. No.
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        in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagno and treatment of colorectal carcinomas and cancers. AAH37196 to AAH372 and AAB77789 represent sequences used in the exemplification of the
                                                                                                        cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat discorders associated with decreased expression by rectifying mutations or deletions
                                                                                                                                                                                                        AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                     Claim 1; Page 3592; 9803pp; English.
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                                                                                                                                                                                                                                                                Nucleic acids encoding useful for preventing,
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                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
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100.0%; Pr
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8.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes cDNA sequences (AAX61322-X61470) encoding human secreted proteins (AAX19442-Y19590). The polynucleotides and their corresponding secreted polypeptides useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the polypeptides in a sample or by determining the presence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
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Florence C, Florence KA, Gr
Lafleur DW, Moore PA, Ni J
, Shi Y, Soppet DR, Wei Y,
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Wei Y, Young P;
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expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developing abnormalities and fetal deficiencies, blood disorders, leukemias,

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Alzheimer's

diseases of the immune system, autoimmune diseases,

inflammation, allergies, ischemic

disease, lymphomas,

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The specification describes cDNA sequences (AAX61322-X61470) encoding human secreted proteins (AAY19442-Y19590). The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly
                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptides they encode
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P-PSDB; AAB66933.
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XX AAX61470:

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XX DA encoding a human secreted protein.

XX Human secreted protein; cancer; tumour; neurodegenerative disorder; tww developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease;

XX renal disease; lymphoma; inflammation; allergy; ischemic shock;

XX renal disease; lymphoma; schizophrenia; prostate disease;

XX lung disease; thymus disease; digestive disorder; endocrine disorder;

XX renal disease; thymus disease; digestive disorder; endocrine disorder;

XX human secreted protein; arthritis; malignancy; testees disease;

XX lung disease; thymus disease; digestive disorder; endocrine disorder;

XX human secreted protein; arthritis; malignancy; testees disease;

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XX human secreted protein; allergy; ischemic shock;

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Patent: WO 9854316-A 3 03-DEC-1998;
PATENT: WO 9854316-A 3 03-DEC-1998;
PATENT: WO 9854316-A 3 03-DEC-1998;
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Voelker, T. Alois, Davies, H. Maelor and Knutzon, D. C8 and C10 medium-chain thioesterases in plants Patent: US 5667997-A 6 16-SEP-1997;

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-MAR-1997) to the DDBJ/EMBL/GenBank databases.
Kiyonobu Ueno, Osaka University Medical School, Department of
Medicine III; 2-2, Yamada-oka, Suita, Osaka, Japan, Suita, Oss
565, Japan (E-mail:ueno-k@kinchu.hosp.go.jp, Tel:06-879-3835,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB002449.1 GI:2943812 advanced lung cancer. advanced lung cancer. advanced tissue_lib:fetal brain cDNA to mRNA, clone:843Ex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB002449 1228 bp mRNA prI 13-FI Homo_sapiens mRNA from chromosome 5q21-22, clone:843Ex
                                                                                                                                                                                                                                                                                                         Fax:06-879-3839)
                                                                                                                                                                                                                                                                                                                                                                                                                       Ueno, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-JUL-1997) to the DDBJ/EMBL/GenBank databases. Shunsuke Imanishi, School of Agriculture, Nagoya University, Laboratory of Biochemistry; Furo-cho, Chikusa, Nagoya 464-01, (E-mail:i45184a@nucc.cc.nagoya-u.ac.jp, Tel:052-789-4098, Pax:052-789-4094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kojima, H., Hashizume, K., Imanishi, S. and Nakamura, K
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Direct Submission
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(bases 1 to 1228)
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                   /tissue_lib="fetal brain"
<1. .>1228
                                                         /map="5q21-22"
                                                                          /chromosome="5"
/clone="843Ex"
                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                       Location/Qualifiers
/note="expressed ubiquitously"
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/db_xref="GI:2280518"
/translation="LELHRGGGRSRTSGSPGLQEFGTSSTFFNRPTGRESNGRVIIDF
/translation="LECHRGGGRSRTSGSPGLQEFGTSSTFFNRPTGRESNGRVIIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Nicotiana tabacum"
/strain="bright yellow 2"
/db_xref="taxon:4097"
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/product="BYJ15"
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LOCUS
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Voelker,T.A. and Davies,H.M.
Medium-chain thioesterases in plants
Patent: US 5455167-A 10 03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 from patent I14842
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Sequence 1
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Coldren,C., Flint,D., Hallahan,D.L.
Cis-prenyltransferases from plants
Patent: WO 0121650-A 1 29-MAR-2001,
E.I. DU PONT DE NEMOURS AND COMPANY
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                                                                                                                                              /organism="unknown"
372 c 429 d
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/db_xref="taxon:13490"
268 c 297 g 386
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7.7e-21
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nes 62; Conserv
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AR060385
                                                                                                                                                                                                                    1 Similarity
58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR070327 2605 bp DNA
Sequence 4 from patent US 5892010.
AR070327
AR070327.1 GI:7221215
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625 c 550 g
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KHERRVKELTYQTEEDRKNVLRLQDLVDKLQSKVKAYKRQAEEAEEQSNVNLAKFRKI
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KEQLAMVERRANLLQAEIEELRATLEQTERSRKIAEQELLDASERVQLLHTQNTSLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="PPGCRNSARGKLEGDLKLAQESTMDVENDKQQLDEKLKKKEFEM
SNLQSKIEDEQALGMQLQKKIKELQARIEELEBEIEAERASRAKAEKQRSDLSRELEE
ISERLEEAGGATSAQIEMNKKREAEFQKMRRDLEEATLQHEATAATLRKKHADSVAEL
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650 c 871 g 398 t
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/protein_id="AAB29713.2"
/db_xref="GI:8250661"
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                                             from patent US 5840568.
               GI:5986835
                                                                 2085 bp
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                                                                                                                                                                                                                                            56;
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                               Nicotiana tabacum (strain:bright yellow 2) Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodgkin's disease associated molecules Patent: US 5840568-A 7 24-NOV-1998;
                                                                          BYJ15
                                                                                    AB005878.1 GI:2280517
                                                                                                   AB005878
                                                                                                             Nicotiana
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76 c 102 g
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/db_xref="taxon:9606"
1. .380
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398 c 557 g
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tabacum mRNA
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Primates;
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Pred. No.
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EMMERMANN MICHAEL (DE); KOSSMANN JENS (DE)
Location/Qualifiers
1. .2307
                                               Spermatophyta: Magnoliophyta: Liliopsida: Poales: clade; Panicoldeae: Andropogoneae; Zea.

1 (bases 1 to 2307)

Romermann, M. and Kossmann, J.

NOVEL NUCLEIC ACID MOLECUES FROM MAIZE AND THEIR PRODUCTION OF MODIFIED STARCH
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PALENT: WO 9827212-A 5 25-JUN-1998;
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Sequence 5 from Patent
A91160
A91160.1 GI:6740195
                                                                                                                                             Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                  Zea mays
                                                                                                                                                                                                   Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1977)

Gu.J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Gin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
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Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.
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Location/Qualifiers
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608 c 605 g
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RYPVILRRFELRRGSGGRGRFRGGDGVTRELLFREEALLSVLTERRAFRPYGLHGGEP
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817. .1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%;
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Pred. No.
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                                                                                 AND THEIR USE FOR
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Best Local
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1036 cc 1037
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Ogata, I., Saez,C.G., Greenwel,P., Ponce M de,L.,
Leinwand,L.A. and Rojkind,M.
Rat liver fat-storing cell lines express sarcomes
chain mRNA and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
S68736
                                                                                                                                                                                                                                                                                                                  GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 143657] from the original journal article. This sequence comes from Fig. 3.
                                                                                                                                                                                                                                                                                                                                                                                              94116097
                                                                                                                                                                                                                                                                                                                                                                                                               Cell Motil. Cytoskeleton 26 (2), 125-132
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/gene="myosin heavy chain, MHC"
/note="MHC: This sequence comes from Fig. 3; concept translation presented here differs from translation publication"
                                                                                                                                                                                                       /db_xref="taxon:10118"
/cell_line="CC14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYDSVPMDEEDEVVLDYTTDPLIVDRGFRSSILSSIARAGHAIEELYGSPQDVEGVVKDGKIYVVQTRPQM"
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LGEIRKVVLNLTAPMQLVNELKERMLGSGMPWFGDEGDRRWEDAMMAIKVMASSKME
RAYFSTRKVKLDHEYLSMAULVQEVVNADYAFVIHTTNPSSGDSSETYAEVVRGLGET
LVGAYPGRAMSFVCKKDDLDSPKLLGYPSKPIGLFIRQSIIFRSDSNGEDLEGYAGAG
                                                                                                                                                          /cell_type="fat storing
/tissue_type="cirrhotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLNRFDPVLRNVAHLGSWQV1SPVEVSGYVVVVDELLAVQNKSYDKPTILVAKSVKG
EEEIPDGVVGVITPDMPDVLSHVSVRARNSKVLFATCFDHTTLSELEGYDQKLFSFKP
TSADITYREITESELQQSSSPNAEVGHAVPSISLAKKKFLGKYAISAEEFSEEMVGAK
                                                                                                             /gene="myosin heavy chain, MHC"
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AKAFLDRNRLALASKGEQYHNMMQPSAEYLGSLLSIDQWAVNIFTEEIIRGGSAATLS
                                                                                                                                                                                                                                                       /organism="Rattus sp."
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/db_xref="GI:6740196"
/translation="HELEGLLEARVELRPLLLDSRERMKDLIFLDIALDSTFRTAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcatgtcagagatcttccctctgcacatcaagggtgtggctaccggcgtctgtqtcctc
                                                                                                                                                                                                                                                                                                                                                                         accaactggttcatggcctttctggtgaccaaagagtttaacagcatcatggagatcctc
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                                                                    AB033418.1 GI:7592743
glucose transporter 8.
Rattus norvegicus cDNA
                          Mammalia; Eutheria;
                                          Rattus norvegicus
Eukaryota; Metazoa
                                                                                                                       AB033418
                                                                                                                                                 Rattus
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Direct Submission
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/product="glucose transporter"
/product="glucose transporter"
/prodein_id="CAB75729.1"
/db_xref="GI:7018605"
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GYSSPAIPSLRTAPPALRLGDTAASWFGAVVTLGAAAGGVLGGWLLDRAGRKLSLLL
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CTVPFYTGFAVITAARDVWMLLGGRLLTGGLAGGVASLVAPVYISEIAYPAVRGLLGSC
VQLMVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMETPTRFLLTQRQUSGVNAL
MAALRFLMGSEEGWEEPPVGAEHQGFQLAMLRRPGVHKPLITGICLMVPGQLGGVNAL
MAALRFLMGSEEGWEEPPVGAEHQGFQLAMLRRPGVHKPLITGICLMVFGN
MFYANTIFEEAKFKDSSLASVTVGILVPISAEPADVHLGLAWLAVGSMCLETAGFAVGWGB
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30. .1466
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                                          Metazoa; Chordata;
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                            Rodentia;
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Pred. No. 9.2e-193;
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, Rue du Bugnon 27, Lausan
                                       Vertebrata;
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                                       Euteleostomi;
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Molecular cloning of a new putative glucose Published only in DataBase (2000) In press 2 (bases 1 to 2189)
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Ibberson,M., Oldry,M. and Thorens,B.
GLUTXI, a novel mammalian glucose transporter expressed
central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                              Rattus norvegicus mRNA for glucose transporter (GLUTX1 gene). AJ245935
AJ245935.1 GI:7018604
glucose transporter; GLUTX1 gene.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AR054175 Sequence
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AJ131096 Picea abi
AX047063 Sequence
BC008364 Homo sapi
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AJ001753 Arabidops
Y11254 O.latipes m
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AR2298 Sequence 1
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AB028859 Homo sapi
Z31401 A.thaliana
AX063691 Sequence
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Best Local Similarity

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                                                                                                                                                                                                                                                                                      Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFZp434P0816) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.0%; Score 380; DB 10; larity 100.0%; Pred. No. 1.2e-87; Conservative 0; Mismatches 0;
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/tissue_type="testis"
/dev_stage="adult"
/lab_host="pH108"
/note="vector: pSport1; Site_1: Not.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 515 Std Error: 0.00

Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                         AI338005 451 bp mRNA
qt35d10 x1 Soares_pregnant_uterus_NbHPU
IMAGE:1949971 3', mRNA sequence.
                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 451)
                                                                                                                                                                  Unpublished (1997)
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National Cancer Institute, Cancer Genome Ana
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                                                                                   Location/Qualifiers
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Primates;
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Koehrer.k
Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz heidelberg.de; sequenced by BMF2 (Biomedical Research Center at the Charite,
                                                                                     Koehrer, K., Beyer, A., EST (Koehrer, et al.) Unpublished (1999)
                                                                                                                                                                                                                         AL041348 389 bp mRNA EST DKFZp434P0816_rl 434 (synonym: htes3) Homo DKFZp434P0816 5', mRNA sequence.
                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa;
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                                                                            Koehrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
AACTGGAARATTCGCGGCCCCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                      GI:5420699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 384; DB 1
Pred. No. 1e-88;
0; Mismatches
                                                                                                               Mewes, H.W.,
                                                                                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                               Gassenhuber, J.
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                                                                                                                                       Hominidae;
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CDNA clone
                                                                                                                                                    Euteleostomi;
                                                                                                               Wiemann,
                                                                                                                                        Homo
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AW955452
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                                                                                   cagagecectgectgeccaggggagecagaatecagececttggagecttggtetgeag 1486
                                          99tccctccttcctgtcatgctccctccagcccatgacccggggctaggaggctcactgc
                                                                                                                                                          cgatgacagccactcactaggggatggagcaagcctgtgactccaagctgggcccaagcc
ctcctgttccagctcctgctgctgctctgaggactcaggaacaccttcgagctttgcaga 1606
                             GGTCCCTCCTTCCTGTCATGCTCCCTCCAGCCCCATGACCCCGGGGCTAGGAGGCTCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggftctacatctccgaaatcgcctacccagcagtccgggggttgctcgggctcctgtgtgc 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGCTGGGGGGCCTCCTCACCGGCCTGGCCTGCGGTGTTGCCTCCCTAGTGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: John Quackenbush
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW955452 651 bp mRNA EST
EST367522 MAGE resequences, MAGD Homo sapiens
AW955452
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quackenbush, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hegde, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW955452.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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gde,P., Qi,R., Abernathy,K., Dharap,S.,
E., Saeed,A.I., Sharov,V., Lee,N.H., Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: Reverse
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                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences,
/note="Vector: pBBluescriptSKm"
185 c 169 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                        Score 390; DB 10;
Pred. No. 2.1e-90;
                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                    Length 651;
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Best Local Similarity
Matches 676; Conserv
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10709 row: p column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 'Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG700749
BG700749.1 GI:13970402
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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segref@genoscope.cns.fr, Web :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Fetal brain; Vector: pCMVSPORT 6: 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the and cloned vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://fulllength.invitrogen.com"
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/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="CSODF005YE02"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 309 c 275 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="melanotic melanoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xho1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4641145"
/clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 2.9e-92;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tegectacecageagteeggggttgeteggeteetgtgtgeagetaatggtegtegteg 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCACCGGCCTGGCCTGCGTGTTGCCTCCCTAGTGGCCCCGGGTCTACATCTCCGAAA
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      (CGAP/BTGAP), Tumor Gene
Unpublished (1998)
Contact: Robert Strausber
                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 442)
NCI/NINDS-GCAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute / National Institute of the Disorders and Stroke, Brain Tumor Genome Anatomy Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW051497 442 bp mrNA EST 09-MAR-2000 wy96bil.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2556381 similar to contains MER22.b2 TAR1 repetitive element;, mRNA
                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                EST
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a 178 c 164 g 93 t 1 others
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/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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QΥ Дb Qy В Qy Ъ Qy Ъ 9 Вb δÃ Вb γQ 밁 24

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                  agctaatggt 435
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                                                           CGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGTTGCTCGGCTCCTGTGTGC
                                                                           cggtctacatctccgaaatcgcctacccagcagtccgggggttgctcggctcctgtgtgc
                                                                                                                           TGCTGCTGGGGGGGCCTCCTCACCGGCCTGGCCTGCGTGTTGCCTCCCTAGTGGCCC
                                                                                                                                          tgctgctggggggccgcctcctcaccggcctggcctgcggtgttgcctccctagtggccc
                                                                                                                                                                                        TGTGCTCCGTGCCCTTCGTGGCCGGCCTTTGCCGTCATCACCGCGGGCCCAGGACGTGTGGA
                                                                                                                                                                                                          tgtgctccgtgcccttcgtggccggctttgccgtcatcaccgcgggcccaggacgtgtgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGCCGCCGTCTTCCTCGCCGCCTTCGCCCTGCCCTGGGCCCACTCAGCTTCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                        TCGCGCTCGGCTACAGCTCCCCGGCCATCCCTAGCCTGCAGCGCGCCGCCCCCCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1636 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2556381"
/clone_lib "NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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/clone="TWACE"
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-100;
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1 (bases 1 to 457)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.cih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Micha
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                             quality sequence stop: 373
Location/Qualifiers
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   25.2%;
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. No.
   DB 10;
2.7e-107;
            Length 457
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                                                                                                                                                                                                   cgapbs-r@mail.nih.gov
/clone="IMAGE:1687085"
                                          Location/Qualifiers
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                                                                                                                               DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1597 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                        Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 464.
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                      cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento
                                                                                                                                                                                                                                                                                                                               Procurement: David N. Louis,
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 bp mRNA EST 01-OCT-1998 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1687085 TR:Q39416 Q39416 INTEGRAL MEMBRANE PROTEIN. ;, mRNA
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tgcctcc 1273
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Plate: LLAM9706 row:
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
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/tissue_type="epithelioid carcinoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
287 g 213 t
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/clone="IMAGE:3903048"
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                                                                                             GAAGAGGCCAAGTTCAAGGACAGCAGCCTGGCCTCGGTCGTCGTGGGTGTCATCCAGGTG
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Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
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Other_ESTs: 2820759.3prime
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National Institutes of Health, Mammalian
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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1 (bases 1 to 932)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602527373F1 NIH_MGC_21 Homo
                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1433 row: a column: 19
                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
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BE910478
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         Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 934) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian (
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/lab_host="DH10B (phage-resistant)"
/not="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Sites using the following of cloned into EcoRI/XhoI sites using the following of adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
06 a 318 c 314 g 194 t
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TGTGCTCCGTGCCCTTCGTGGCCGGCTTTGCCGTCATCACCGCGGCCCCAGGACGTGTGGA
                                                                             c999999agtgctggctggctggtggaccgcgcgggcgaagctgagcctcttgc
                                                                                                                      CGCGCCTGGACGACGCCGCCGCCTCCTGGTTCGGGGCCTGTCGTGACCCTGGGTGCCGCGG
                                                                                                                                                                                                                                                                                                               592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM10769 row: h column: 02
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National Institutes of Health, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
1 (bases 1 to 879)
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for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Li constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Lib a 319 c 296 g 169 t
                                                                                                   /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BanHI; Site_2: SalI XhOI (gtc; ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3' size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length of the format of the second contents.
                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                     /clone="IMAGE:4837297"
/clone_lib="NIH_MGC_97"
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                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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clone IMAGE:4837297
                        NIH_MGC Library."
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Matches 576; Conserv

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Score 576; DB ; Pred. No. 7.9 0; Mismatches

7.9e-138; DB 11;

Length 879;

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TITLE
JOURNAL
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 source
        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1681 row: p column: 12
High quality sequence stop: 745.
Location/Qualifiers
                                                                                                                                                                                                                  Eukaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 949)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                    HYPOTHETICAL:
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NAME: PADST, PATTREA L.
REGISTRATION UMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Massachusetts Institute Of Technology TITLE OF INVENTION: DNA Encoding the Heme-Regulated TITLE OF INVENTION: Eukaryotic Initiation Factor 2
                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                              NAME/KEY:
LOCATION:
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                             OTHER INFORMATION:
                                                                                              OTHER INFORMATION:
                                                                                                                                                           CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            NAME/KEY:
                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/08131
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: 7729-7733
September-1991
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                                                                                                                                                                                                                                                                                                                    2729 base pairs
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1100 Peachtree Street
                                                                                                                                                                                                                          NO
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404-815-6555
                                              misc_feature
229..249
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113..2149
misc_feature
                                                                                                                                                                             Rabbit
                                                                                                                                                                                                                                                                         linear
                                                                                                                                                          Reticulocytes
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100.0%; Pr
170 0;
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Pred. No.
                          "Primer used in the amplification of human HRI cDN
                                                                                         "Expression of HRI mRNA in Human erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                    5807
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Job time:

Search completed: February 13,

2002, 20:05:17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-08131-1
                                                       Query Match 1.2%; Score 22; Best Local Similarity 100.0%; Pred. No. Matches 22; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09306290 Patent No. 6221635
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                   APPLICANT: Rovera, Giovanni
APPLICANT: Mukhopadhyay, Sunii
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
FILE REFERENCE: 09924-10
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/306,290 CURRENT FILING DATE: 1999-05-06 NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                               LENGTH: 43
               1788 aatcaaaaaaaaaaaaaa 1809
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 24
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
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AATCAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homology to yeast GCN2 protein kinase and human double-stranded-RNA-dependent
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . London, Irving M.
Cloning of the cDNA of the heme-regulated eukaryotic initiation factor 2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
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1009..1031
                                                                                                                                                    Description of Artificial Sequence: Primer {\tt RH598}
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                    GENERAL INFORMATION:
                                                               APPLICANT: Chen, Jane J.

APPLICANT: London, Irving M.

TITLE OF INVENTION: DNA Encoding the Heme-Regulated

TITLE OF INVENTION: Eurkaryotic Initiation Factor 2
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS: London, Irving M.

TITLE: Cloning of the cDNA of the heme-
TITLE: regulated eukaryotic initiation factor
TITLE: 2alpha (EIF-2alpha)kinase of rabbit reticulocytes:
TITLE: 2alpha (EIF-2alpha)kinase and human
TITLE: Homology to yeast GCN2 protein Kinase and human
TITLE: double-stranded-RNA-dependent
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                         ADDRESSEE:
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DATE: September-1991
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LOCATION: 448.468
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                                                                                                                                                                       , Application US/08630524 5690930
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: Patrea L. Pabst
2800 One Atlantic Center
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543..560
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229..249
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113..2149
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amplification of a human HRI cDNA sequence
using the rabbit HRI cDNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Primer used in the amplification of human HRI cDNA sequence using the rabbit HRI cDNA sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using the rabbit HRI cDNA sequence
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                       Pabst
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                                                                             alpha kinase
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TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION: 543..560
OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                     PUBLICATION INFORMATION
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                AUTHORS:
AUTHORS:
TITLE: C
                                                                                                                                        NAME/KEY:
                                                                                      OTHER INFORMATION: /note= "Primer used in the OTHER INFORMATION: amplification of a human HRI cDNA sequence OTHER INFORMATION: using the rabbit HRI cDNA sequence."
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 448..468
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regulated eukaryotic initiation factor
                  Cloning of the cDNA of the heme
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                                   London,
                                                    Chen, Jane J
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113..2149
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543..560
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229..249
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                                                                                                                                                                                           /note= "Primer used in the
amplification of human HRI cDNA sequence
using the rabbit HRI cDNA sequence."
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mRNA in Human erythroid cells, using as
probe rabbit HRI cDNA from nucleotides
to 2149."
                                                                                                                                                                                                                                                                                                     amplification of human HRI cDNA sequence using the rabbit HRI cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Primer used in the amplification of human HRI cDNA sequence using the rabbit HRI cDNA sequence."
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US-09-665-309-7
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-664-800-7
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; ORGANISM: Arabidopsis thaliana
US-09-416-050A-7
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US-09-664-800-7
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Best Local Similarity
                                                                  Matches
                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: KIM. Soo Young
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SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 1942/42
CURRENT APPLICATION NUMBER: US/09/664,800
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR FILING DATE: 1999-10-12
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Patent No. 6218527
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/665,309 CURRENT FILING DATE: 2000-09-19
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                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
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1702 aaatcaaaaaaaaaaaaaaaa 1724
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                                                                 Conservative
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100.0%; Pred. No. 1.7
Tative 0; Mismatches
                                                                             1.3%; Score 23; DB 4; 100.0%; Pred. No. 1.7;
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US-07-938-782A-1
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Best Local Similarity
Matches 23; Conserv
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SEQ ID NO 7
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                                                                                                                                                                 FILING DATE: 31-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404,873-8794
                                                                                                                 TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/416,050
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: London, Irving M.

TITLE OF INVENTION: DNA Encoding the Heme-Regulated
TITLE OF INVENTION: Eurkaryotic Initiation Factor 2 alpha kinase
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MOLECULE TYPE:
HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
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                                      TOPOLOGY:
                                                    STRANDEDNESS:
                                                                                            LENGTH:
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ZIP: 30309-3450
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STATE: Georgia
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STREET: 1201 West Peachtree Street
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                                                    nucleic acid
EDNESS: single
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                                                                                            2729 base pairs
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                  CDNA
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1999-10-12
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100.0%; Pred. No.
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; LOCATION:
US-08-168-091A-1
                                                                     US-08-076-011-1
                                                                                                                                                                                                                                                              TOPOLOGY: US-08-697-954-1
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                           Sequence 1, Application US/08076011 Patent No. 5521069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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1185 Avenue of the Americas
ONDA, Haruo
KIMURA, Chiharu
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                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                  1.3%; Score 24;
100.0%; Pred. No.
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100.0%; Pred. No.
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0.66;
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0.68;
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; LOCATION:
US-08-076-011-1
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KIM. Soo Young
             SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                             Sequence 7, Application US/09416050A Patent No. 6194559
                                             TITLE OF INVENTION: Abscisic Acid Responsive FILE REFERENCE: 1942/42 CURRENT APPLICATION NUMBER: US/09/416,050A CURRENT FILING DATE: 1999-10-12 NUMBER OF SEQ ID NOS: 83
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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LENGTH: 1737
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: RESNICK, DAVID S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,676
FILING DATE: 07-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,246
FILING DATE: 13-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                       220 TCAAAAAAAAAAAAAAAAATTCC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 11-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17041 base pairs
TYPE: nucleic acid
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                                FastSEQ for Windows Version 4.0
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11602..11787)
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100.0%; Pred. No.
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0.56;
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US-08-568-147B-1
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APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Katsumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAM
TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
TITLE OF STOHENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-JAN-1993
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 800,952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1786 aaaatcaaaaaaaaaaaaaaaaa 1809
                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 6.1
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APPLICATION NUMBER: 07/965,273
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                                       CLASSIFICATION:
                                                        FILING DATE:
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                           COUNTRY: US
ZIP: 11530
                                                                                                                                                                                                                                                              STREET: 400 Garden City Plaza CITY: Garden City
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nes 24; Conserv
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                                                                                                                                                                                                                            USA
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REYMOND, CHRISTOPHE DOMINIQUE
                                                                                                                                                                                                                                                                                               Scully, Scott, Murphy & Presser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                       DNA FRAGMENT CODING FOR SQUAMOUS CELL
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                                                                        US/08/568,147B
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US-08-168-091A-1
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Best Local Similarity
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                                                               INFORMATION FOR SEQ ID NO:
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                             SEQUENCE CHARACTERISTICS:
LENGTH: 2351 base pairs
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
FILING DATE: 29-SEP-1992
                                                                            REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1711 base pairs
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NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 15-DEC-1993
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
STRANDEDNESS:
                  TYPE:
                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                              NAME:
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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CITY: Boston
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STRANDEDNESS: both
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             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                          ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fischbach, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.
                                                                                                                                           31,503
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RESULT 1
US-08-574-959A-3
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; Patent No. 5962224
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                                                                                                                                                                REFERENCE/DOCKET NUMBER: DFN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSOMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0:
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy I
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                        FEATURE:
NAME/KEY:
                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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STREET: 60
CITY: Bost
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COUNTRY:
                                                                                                                 TOPOLOGY:
                                                                                                                             STRANDEDNESS:
                                                                                                                                                    TYPE:
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US-08-48-360-21
US-08-646-360-21
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PCT-US94-05407-10
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US-08-955-902-40
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GENERAL INFORMATION:
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US-08-451-405A-2
; Sequence 2, Application US/08451405A
; Patent No. 5736338
                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-357-014-3
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US-09-357-014-3
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                                                                                                                                                                   Matches 26;
                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                     1939
                                                                                                                     1788 aatcaaaaaaaaaaaaaaaaaaattcc 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-U1-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/574,959
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                    AATCAAAAAAAAAAAAAAAAATTCC 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 60 State Street, Suite 510 CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                  LOCATION:
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                                                     Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1785 gaaaatcaaaaaaaaaaaaaaaaa 1809
                  or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                    New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacteria; antifugal; antiparasitic; cardiant; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
                                                                                                                                                                                                 Claim 1; Page 555; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human breast and ovarian cancer associated antigen gene SEQ ID
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DB; AAB58808.
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                                                         protein, agonist
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                                                                                                                                                                                                   arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
                                                                                                                                                                                                                                              antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
                                                                                                                                                   Sequence
                                                                                                                                                                                   cerebral anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                  diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
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                                                           Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatord arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune
                                                                                                                                                                              Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 224 and 239 polypeptides useful for the treatment of asthma, rharthritis, psoriasis and autoimmune diseases
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cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes;
systemic lupus erythematosus; transgenic animal; diagnosis;
prognosis; prophylatic; therapeutic; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO: 128, 140: 197; 212; 213; 224; 239; modulating agent; agraft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel diseases; septic shock; ulcerative colittis; Crohn's disease; chronic myelogenous leukemia; cancer; liver
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            transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in
                                     diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for produc
                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                    versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease,
                                                                                                                                                                                                Nucleic acids encoding TANGO polypeptides are useful as mod agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, influences
                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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systemic lupus erythematosus; transgenic animal;
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/product= TANGO 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               992 A; 733 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
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                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3413
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                        as modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 197, 212, 213, asthma, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune

erythematosus.

e.g. myasthemia gravis,

The nucleic acids are also

autoimmune diabetes

for

producing

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AAF12939
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Best Local
The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative expression of the same genes in one or more second filamentous fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus prisarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichderma reesei, which are
                                                                                                                                                                                            Monitoring differential expression of genes in uses fluorescence-labeled nucleic acids isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1789 atcaaaaaaaaaaaaaaaaaaaattcc 1813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae
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nes 25; Conser
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                                                                                                                                                                                                                                                                                                                                       RM,
                                                                                                            88; Page 2271-2272; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                 Rey MW,
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                                                                                                                                                                   expressed sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engineering; catabolic pathway engineering; ss
                                                                                                                                                                                                                                                                                                                                 Shuster JR,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                 Kauppinen S,
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                                                                                                                                                                                                                                                                                                                               IG,
                                                                                                                                                                                       s fungal cells
cells and a
                                                                                                                                                                                                                                                                                                                               Olsen
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B

The present sequence encodes a human tumour suppressor, designated enhancer of polycomb (Epc). Human Epc genes can be used to identify p10-11 region of human chromosome 10 and a q13.3 region of human chromosome 22. The Epc genes and expression products are useful as

Claim 15; Page

50; 55pp; English

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RESULT
AAX83994
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Best Local
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                                                                                                                             Mammalian tumour suppressor, termed enhancer of polycomb, useful for therapy, prognosis and diagnosis of proliferative and developmental
                                                                                                                                                                                   WPI; 1999-419108/35
                                                                                                                                                                                                                    Randazzo
                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                    28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPC1; EPC2; enhancer of polycomb; tumour suppressor; diagnosis;
proliferative disorder; developmental disorder; neoplasia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human EPC1 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
                                                                                                                                                                                                                                                                                      30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                      WO9933986-A1
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the global expression of genes from FF cells allows the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suppressor genes. (1), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (1) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (1)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations). AAH81492-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                 are
                                                            The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs
                                                                                                                                                               Claim
                                                                                                                                                                                             Monitoring differential expression of genes uses fluorescence-labeled nucleic acids isol substrate of expressed sequence tags -
                                                                                                                                                                                                                                                            WPI;
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                  same genes
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                            e FF cells and a substrate of expressed sequence tags (EST). e used in the methods for monitoring differential expression a first filamentous fungal (FF) cell relative to expression
global
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NORDISK
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                                                                                                                                                                                                                                                                                            Shuster
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Pred. No.
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                                                                                                                                                                                                            enes in filamentous fungal cells isolated from the cells and a
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culture condition;

metabolic pathway engineering;

environmental stress; spore morphogenesis; engineering; catabolic pathway engineering;

Aspergillus oryzae.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses filorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs

genes

Claim

88; Page 2269-2270;

3161pp;

English.

Monitoring differential expression of genes uses fluorescence-labeled nucleic acids iso substrate of expressed sequence tags -

enes in filamentous isolated from the c

s fungal cells an

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2000-594572/56

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22-MAR-1999; 22-MAR-2000; 28-SEP-2000

99US-0273623

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AAF12934/c
ID AAF12934
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1789
                                                                                                                                                                                                                                                                                                                                                                                      Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovered, possible functions of unknown open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potential of the microorganisms to be improved. New genes may be
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Best Local Similarity
cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation, e.g. for treatment of tumours \left(\frac{1}{2}\right)^{2}
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                                                                                                            WPI; 1997-341351/31.
P-PSDB; AAW31183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 1977 BP
                                                                                                                                                                                            Strominger JL,
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7.2e-06;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA sequence encodes a novel p62 cytoplasmic polypeptide which has 77.5 per cent homology to the nucleic acid sequence of p62 represented in AAT89343. This cytoplasmic polypeptide is expressed in B cells and other cells of haematopoietic origin e.g. T cells. p62 is capable of modulating T or B cell development and/or T or B cell activation e.g. by modulation of Lck activity. It is also capable of modulating degradation of cellular proteins e.g. cell cycle repulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p62 acts to boost B cell response and may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1939 aatcaaaaaaaaaaaaaaaaaattcc 1964
                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                       Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV infection. Inhibitors of p62 can be used to reduce B or T cell responses and may be used to treat a variety of autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple sclerosis allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microorganisms, e.g. bacteria, viruses and protozoans. p62 can be used to expand T cell populations for treating infectious diseases or cancer, e.g. the resulting cells may be transduced to render them resistant to
                                                                                                                                                                                                                                                       31-JAN-2000; 2000DE-1004102
                                                                                                                                                                                                                                                                                     31-JAN-2001; 2001WO-EP01003
                                                                                                                                                                                                                                                                                                                                                                            Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH82014 standard;
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                                                                                                                   Nucleic acids
                                                                                                                                                  WPI; 2001-483415/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat differential transcription-associated cDNA
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                                                                                                                                                                                                                          (META-) METAGEN GES GENOMFORSCHUNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treat disorders where this is beneficial, e.g. infections by pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aatcaaaaaaaaaaaaaaaattcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Fig 3; 175pp; English.
                                                                                                   for diagnosis
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                                                                                                                                                                             A, Hinzmann B,
Hellriegel M,
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                                                                                                  differentially expressed agnosis or therapy of tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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                                                                                                                                                                             Schmefer R, Zuber J, Schmitz A, Sers C;
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This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour

Claim 6;

Page 513; 579pp; German

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and terrial infections becterial, fungal or viral infections.
                                              Murine; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anticonvulsant; and antidepressant. The sESTs can be used for generated and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                           Murine
                                                                                                                                                                                                                                                       17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                   AAF55867 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease), tumours, bacterial, fungal or viral infections, depression psoriasis. AAA45926 to AAA45931 represent linker variants which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules which correspond to the sESTs. Proteins encoded by the sESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
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Pred. No. 6.9e-44;
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Best Local (
                          14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention reatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a hyperglycaemia disease. The present sequence is the coding sequence
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                                                                                                                                                                                                               14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat GLUTX1
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13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequence
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99US-0151140.
2000US-0184285.
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The present sequence is human protein with hydrophobic domain encoding CDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional activity. The polypeptides and nucleic acids may be used as nutritional
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11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate activing and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 287-289; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins with hydrophobic domains them, useful for preventing diagnosing alzheimer's and inflammation -
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                                                                                                                                                                                                                                                                                                                        thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
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RESULT AAD12574 ID AAD1 XX AC AAD1 XX AC AAD1 XX DT 25-S XX DE Huma

AAD12574

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Human 25-SEP-2001

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Qy В γQ

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relates

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GLUTX

proteins

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RESULT
AAF55865
ID AF5
XX AAF5
AC AAF5
AC AAF6
XX Huma
AKW Huma
KW Huma
KW hypo
OS Homc
XX Homc
XX Homc
XX Hom
PD 18-0
PD 18-0
XX 14-0
PR 27-1
PR 27-1
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XX UU1
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## ALIGNMENTS

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Human: transporter and ion channel-1; TRICH-1; vaccine: cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epileps; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; chemmatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's Syndrome; Systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.
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Query Match
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Length 2080; Indels

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disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scheroderma, Sjogren's syndrome, systemnic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
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02-FEB-2000;
10-FEB-2000;
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Ibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammalian glucose transporter expressed in central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
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IPWLLMSEIFPLHIKGVATGVCVLTNWFMAFLVTKEFNSIMEILRPYGAFWLTAAFCI
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Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology
Submitted (02-SEP-1999) Ibberson M.R., Rue du Bugnon 27, Lausann
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GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
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GYSPATPTGTAVTTAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSC
                                                                                                                                                                                                                                      SAFGTYFKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSMCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL
SVLFTLTVVPETKGRTLEQVTAHFEGR"
                                                                                                                                                                                                                                                                                      VQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHQYQEA
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MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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SVLFTLTVVPETKGRTLEQVTAHFEGR"
3 673 C 584 g 464 t
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21. .1454
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9e-15;
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9e-15;
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGC
                                                                                                                               Thorens,B., Ibberson,M. and Uldry,M. Glutx polypeptide family and nucleic Patent: WO 0104145-A 3 18-JAN-2001;
                                                                                                               Patent: WO 0104145-A 3 18-J
University of Lausanne (CH)
                                                                                                                                                                                                                                                                                                                        Sequence 3
AX076669
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                        Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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CVAPSFMLLLMCFMPETPRFLLSQVVMVFSTSAFGTYFKLTEGGFSNSSHVDLDALVSM
LETATAALIMDRAGRRLLLTLSGVVMVFSTSAFGTYFKLTEGGFSNSSHVDLDALVSM
                            /db_xref="taxon:10118"
30. .1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAFLVTKEFSSLMEVLRPYGAFWLASAFCIFGVLFTLACVPETKGKTLEQITAHFEGR
          /note="unnamed protein
                                                             /organism="Rattus sp."
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            product"
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J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                  1 (bases 1 to 1843)
Carayannopoulos,M.O., Chi,M.M., Cui,Y., Pingsterhaus,J.M., McKnight,R.A., Mueckler,M., Devaskar,S.U. and Moley,K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057 Aachen, FRG
glucose uptake in the blastocyst
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                  is a glucose transporter responsible for insulin-stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="glucose transporter 8"
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/db_xref="G1:7689220"
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CTVPFVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSC
VQLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHQYQEA
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499 c 438 g 331 t
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PWLLMSE1FPLHVKGVATG1CVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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26. .1459
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/db_xref="taxon:10090"
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. 9.3e-15;
                                                                                                                                                                                                                                     mRNA, complete cds:
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REFERENCE
AUTHORS
TITLE
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SOURCE
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Best Local
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Submitted (07-FEB-2000) OB/Gyn,
Submitted (07-FEB-3000) OB/Gyn,
Of Tonis MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5
AX076671
                                                                                                                                                                                                                                                                                                                      Glutx polypeptide family and nucleic acids Patent: WO 0104145-A 5 18-\mathrm{JAN}-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
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                                                                                                                                                                                                                                                                                                        University of Lausanne
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                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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                                                                                                                                                                     /codon_start=
                                                                                                                                                                                        /note="unnamed protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="glucose transporter GLUT8"
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                                                                                                                                                                                                                          /db_xref="taxon:10095"
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Eutheria;
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Om Patent W00104145.
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Rodentia;
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Pred. No.
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Sciurognathi;
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9.1e-15;
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thi; Muridae; Murinae; Mus
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                                                                                  CGAGCTTTGCAGACCTGCGGTCAGCCCTCCATGCGCAAGACTAAAGCAGCGGAAGAGGAG 6332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccattttgaggggcgatgacagccactcactaggggatggagccaagcctgtgactccaag 1413
                   9t999cctctaggatctttgtcttctggctggaggtgcttttg 1696
                                                                                                                                                                                                       ggaggctcactgcctcctgttccagctcctgctgctgctctgaggaactcaggaacacctt 1593
                                                                                                                                                                                                                                                                                                   ctgggcccaagcccagagcccctgcctgccccaggggagccagaatccagcccctttggag 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccttttcactttgttctgtgtccctgaaactaaaggaaagactctggaacaaatcacagc 1353
GTGGGCCTCTAGGATCTTTGTCTTCTGGCTGGAGGTGCTTTTG
                                                                                                                                                                              GGAGGCTCACTGCCTGCTTCCAGCTCCTGCTGCTGCTGCTGAGGACTCAGGAACACCTT
                                                                                                                                                                                                                                                                           CCATTTTGAGGGGGGATGACAGCCACTCACTAGGGGGATGGAGCAAGCCTGTGACTCCAAG 63084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTTTCACTTTGTTCTGTGTCCCTGAAACTAAAGGAAAGACTCTGGAACAAATCACAGC 63024
                                                                                                                                                                                                                                                                                                                                                                       CTGGGCCCAAGCCCAGAGCCCCTGCCTGCCCCAGGGGAGCCAGAATCCAGCCCCTTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISSPROT: Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP11-356B19 is from the library RPCI-11.2 constructed by the of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: pBACe3.6
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/db_xref="taxon:9606"
/chromosome="9"
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/clone_lib="RPCI-11.2"
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Pred. No. 8e-233;
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                                           G20347 120 bp
human STS A005N15, se
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G20347.1 GI:1340684
                                                                                                                                                                                                                                                       Prepared
                                                                                                                                                                                                                                                                                                                                   Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer A: AAGTCTTTATTTTGGCAAAC
Primer B: CCTCTAGGATCTTTGTCTTC
STS size: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic 9712 Medical Center Dr., F
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS; STS sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                         Protocol:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
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                                                                                       Conservative
                                                                                                                                                        39
                                                                                                                                                                                                                                             with primer pairs derived R17700, T59518, T59564.
                                                                                                                                                     complement(101. .120)
a 36 c 26 g
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KCl: 500 n
MgCl2: 20 n
Triton X-100: 1%
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/db_xref="taxon:9606"
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TaqStart Ab:
Total Volume:
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Kato, S. and Kimura, T.
Human proteins having hydrophobic domains and dnas encoding these
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                               Conservative
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                                                                                                                                  CSVPFVAGFAVITAAQDVWMLLGGRLLITGLACGVASLVAPVYISEIAYPAVRGLLGSC VQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA APGLVRCGHGVQHECLRRLLQADPGWPWQLLARGHLGACLCTAC"
                                                                                                                                                                                GYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLL
                                                                                                                                                                                          /protein_id="CAC51153.1"
/db_xref="GI:15209698"
/translation="MTPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFAL
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                  only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                    on Apr 26, 2001 this sequence version replaced gi:13277497. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone.
assembly was confirmed by restriction digest. abbreviations are used to associate primary a
                                                                                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk
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                                                                             Conservative
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                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
296 c 259 g 15
                                                                                                                                                                          Inc. (JP) ; SAGAMI Location/Qualifiers
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Y17801
Y17801.1 GI:
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GLUTB, a novel member of the sugar transport
with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
                                                                                                                                                                                    Direct Submission
Submitted (16-JUL-1998) H.
Toxicology, Technical Unive
Aachen, FRG
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20283667
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1 (bases 1 to 1508)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                 sapiens
/gene="GLUT8"
27. .1460
                                                                                                                          /tissue_type="testis"
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                                                                                                                                             /organism="Homo sapie
/db_xref="taxon:9606"
                                                                                                                                                                           Location/Qualifiers
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Machen, Wendlingweg 2, D-52057
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CGGGGGGAGTGCTGGCGGCTGGCTGGTGGACCGCGCGCGGGCGCAAGCTGAGCCTCTTGC
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Thorens, B., Ibberson, M. and Uldry, M
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a 750 c 672 g 475 t
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Eutheria;
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Primates;
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                                                          Homo sapiens mRNA for
AJ245937
AJ245937.1 GI:701830
glucose transporter;
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1873)
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nsporter; GLUTX1
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GLUTXI, a novel mammalian glucose transporter central nervous system and insulin-sensitive to J. Biol. Chem. 275 (7), 4607-4612 (2000)
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1005, SWITZERLAND
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Y17801 Homo sapien
AX191497 Sequence
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AL445222 Human DNA
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; MOLECULE TYPE:
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US-09-516-493-7 x US-09-040-444-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and Nor Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 2481.1453-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                       424 CTGGGTCCCTGCCAGGATGGCTGGGTG
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 I S
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.C.
                                                                                                                                                                                to: US-09-040-444-5 from: 1 to: 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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0.946
49.893
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                                                                                                                                                                                                                                                                                          Length: 467
Gaps: 15
Percent Identity: 23.555
                                                                                       ....TATGACACGCCCGGCTC 467
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337	lyGlyProGlyAsnSerSerHisValAlaIleSerAlaProValSerAla	321
1308	G	1308
321	${\tt lMetValPheSerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnG}$	304
304 1307	IleMeAaspArgAlaGlyArgArgLeuLeuValLeuSerGlyValVa ::::::::::::::::::::::::::::::::::	288 1258
287 1257	erValValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeu ::: :::::::::::::::::::::::::::::::::	271 1208
	rAlaGluThrIlePheGluGluAlaLysPheLysAspSerSerLeuAlaS :::     :::     GGGGCTCATCCTGCACATGGGCGCCACCAGCGGGAACCTCTACCTGGATT	254 1158
	SerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPheTy :::::         ::::::        ::::::	238 1120
237 1119	euAlaLeuLeuArgGlnProGlyIleTyrLysProPheIleIleGlyVal     :::        :::      CAGACCTGTTCCGCACGCCGCGCCTGAGGAAGCGCACCTTCATC	221 1076
221 1075	TrpGluAspProProIleGlyAlaGluGlnSerPheHisL                 CCTTTCCCTCGAAGAGGATGTCACCGAAAAGCTGAGCCCTTCATTTG	208 1029
207 1028	PheLeuTrpGlySergluGlnGly	200 979
199 978	roArgPheLeuLeuThrGlnHisArgArgGlnGluAlaIleAlaLeuArg       :::     :::      :::	183 929
183 928	SValProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrP:::         :::       :::       :::	166 879
166 878	TyrLeuAlaGlyTrpValLeuGluTrpArgTrpLeuAlaValLeuGlyCy	150 829
149 828	euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAla :::::           :::	134 779
134 778	LAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL::::        ::      ::::       :::     :::	117 729
117 728	LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa 	101 679
100 678	hrAlaAlaGlnAspValTrpMetLeu ::   ::::	92 629
92 628	USerLeuLeuCysSerValProPheValAlaGlyPheAlaValIleT	75 603
75 602	AlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLe	59 553
58 552	SPASPAlaAlaAlaSerTrpPheGlyAlaValValThrLeuGlyAlaAla	42 518

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08035928 Patent No. 5538844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1421 TGGTGAATGCTGAGCTGTACCCCACATTCGTCAGGAACCTCAGAGTGATG 1470
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                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 ValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeuVa 400
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gusella, James F.
TITLE OF INVENTION: A No. 5538844el Transport Protein Gene
TITLE OF INVENTION: the Huntington's Disease Region
                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 19930:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                LENGTH: 1788 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
TOPOLOGY:
                                                                                                                                                                                  TELEPHONE:
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Y: U.S.A.
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                                                                                                                                                           (202) 833-8716
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MacDonald, Marcy E.
linear
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US-08-035-928-1
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 CGCCGCGTGGTCATCGTTGTCTTT
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                                                                                GCCTCCGAC....CTGCTGTTCATCTTCTGCTTCCTGCCAGAGACG.... 795
                                                                                                                   lProProSerLeuMetLeuLeuMetCysPheMetProGluThrProA 184
                                                                                                                                                             GAGCCTCCCTGCCCCTGGAAATGGCACCCTGGTTTGCCCTGCTCTTCGCA 753
                                                                                                                                                                                                                                                GGTCATTGGGGTGGCCTTCTCACTGGGCTTCACCCTGGGCCCTATGCTCG
                                                                                                                                                                                                                                                                                                                                                                 AlaTyrProAlaValArgGlyLeuLeuGlySerCysValGlnLeuMetVa 142
                                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaCysGlyValAlaSerLeuValAlaProValTyrIleSerGluIle 125
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.CTGCCCCTGGAGAAACGGGCGCCCTCTATCGCCCTGGGGTTC 837
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seq_documentation_block:
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  GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                     Patent No.
                                                                                                                                                                Sequence 42,
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                                                                                                                                     2, Application US/08447430A
5916558
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Recombinant polypeptides and peptides, nucleic acids coding for the same and use of polypeptides and peptides in the diagnostic c
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Quality:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                               2966 CTATICGACTACGCGATCATGGCGACCACCCCGTCCTGTGGATCCTCTAC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                           102 GlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuValAl 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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lLeuGlyCysValProProSerLeuMetLeuLeuMetCysPheMetP 180
                                             GCCGGGGGACTGTTGGGCGCCATCTCCTTGCATGCACCATTCCTTGCG...
                                                                      LeuAlaTyrLeuAlaGlyTrpVal...LeuGluTrpArgTrpLeuAlaVa
                                                                                                                                 TCGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTG
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                                                                                                                                                                                                                   Sequence 40, Application Patent No. 5916558
                                                                                                                                                                                             GENERAL INFORMATION:
                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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                        COMPUTER READABLE FORM:
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                                                 NUMBER OF SEQUENCES:
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                                                              nucleic acids coding for the same and use of these polypeptides and peptides in the diagnostic of tuberculosis.
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alignment_scores:
Quality:
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INFORMATION FOR SEO ID NO: 40
SEQUENCE CHARACTERISTICS:
LENGTH: 3423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                     102 GlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuValAl 118 :::|||||||:::::: ||||
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                                                                                                                                                                                                                                                                                                                                                          aProValTyrIleSerGluIleAlaTyrProAlaValArg............ 131
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                                                                                                                                                                                                                                                       ..GlyLeuLeuGlySerCysValGlnLeuMetValValValGlyIleLeu 147
                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGACGCATCGTGGCCGGCATCACC...GGCGCCACAGGTGCGGTTGC
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roGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaIle 196
                                              ....GCGGCGGTGCTCAACGGCCTCAACCTACTACTGGGCTGCTTCCTA. 2795
                                                                               1LeuGlyCysValProProSerLeuMetLeuLeuLeuMetCysPheMetP
                                                                                                                                       GCCGGGGGACTGTTGGGCGCCCATCTCCTTGCATGCACCATTCCTTGCG.. 2840
                                                                                                                                                                               LeuAlaTyrLeuAlaGlyTrpVal...LeuGluTrpArgTrpLeuAlaVa 163
                                                                                                                                                                                                                                TCGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTG
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seq_documentation_block:
; Sequence 41, Applicati
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                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/08447430A Patent No. 5916558
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                           TITLE OF INVENTION: F
TITLE OF INVENTION: F
TITLE OF INVENTION: F
TITLE OF INVENTION: I
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               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2348 TGACGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCC 2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AlaValGlyTrpGlyProTleProTrpLeuLeuMetSerGluIlePhe 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....SerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyPro 323
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......CGGGGCATGACTATCGTCGCCGCACTTATGACTGTC 268
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                                                                                                                                                                   Recombinant polypeptides and peptides, nucleic acids coding for the same and use of polypeptides and peptides in the diagnostic cuberculosis.
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                       Version
                  #1.25 (EPO)
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alignment_block:
US-09-516-493-7 x US-08-447-430A-41/rev
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                                                                                                                                                                                                                                                                                                                  LeuAlaTyrLeuAlaGlyTrpVal...LeuGluTrpArgTrpLeuAlaVa 163
                                                                                                                                                                                                                                                                                                                                                                         TCGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aProValTyrIleSerGluIleAlaTyrProAlaValArg...... 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATCGACTACGCGATCATGGCGACCACCCCGTCCTGTGGATCCTCTAC 3088
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AlaLeuArgPheLeuTrpGlySerGluGlnGlyTrpGluAspPro...Pr
                                                                                                                                                                                                           lLeuGlyCysValProProSerLeuMetLeuLeuMetCysPheMetP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCGCCTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACT
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                                                                                                       roGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaIle 196
                                               .....ATGCAGGAG.....
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Ratio:
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838	TCGCATAAGGGAGAGCGTCGACCGATGCC 2	2810
212	oIleGlyAlaGluGlnSerPheHisLeuAlaLeuLeuArgG 2	26
809	CTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCG	2770
226	lnProGlyIleTyrLysProPheIleIleGlyValSerLeuMetAla 2	241
769	69	2734
242	PheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAl 2	255
733	TTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGG 2	2689
255	aGluThrilePheGluGluAlaLysPheLysAspSerSer 2	868
883		2643
269	LeuAlaSerValValValGlyValIIeGlnValLeuPheThrAla 2	83
642	GCCTGTCGCTTGCGGTATTCGGAATCTTGCACGCCTCGCTCAAGCCTTC 2	2593
284	ValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuLeuVal 2	999
592	GICACTGGTCCCGCCACCAAACGTTTCGGCGAGAAGCAGGCCATTATCGC 2	543
300	LeuSerGlyValValMetValPheSerThr. 3	909
542	CGGCATGGCGGCCGACGCGTGGGCTACGTCTTGCTGGCGTTCGCGACGC 2	2493
310	SerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyPro 3	123
492	GAGGCTGGATGCCCTTCCCCATTATGATTCTTCTCCCCTTCCGGCGCATC 2	2443
324	GlyAsnSerSerHisValAlaIleSerAlaProValSerAlaGlnProVa 3	340
442	GGGATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGA 2	2402
340	lAspAlaSerValGlyLeuAlaTrpLeuAla 3	350
401	TGACGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCC 2	352
351	ValGlySerMetCysLeuPheIleAlaGlyPhe 3	861
351	TAACTTCGATCACTGGACCGCTGATCGTCACGGCGATTTATGCCGCCTCG 2	302
362	AlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGluIlePhe 377	
301	GCGAGCACATGGAACGGGTTGGCATGGATTGTAGGCGCCGCCCTATAC 225	4

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gb_est2:BF207033
gb_est2:BF410069
gb_est2:BF410670
gb_est1:BE261639
gb_est2:BF401300
gb_est2:BF774206
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gb_est2:BG771736
gb_est2:BG717034
gb_est2:BG281777
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gb_est1:AW055123
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Database length: 1077921985
Search time (sec): 2636.270000
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Query: US-09-516-493-7
Query length: 453
Database: EST:*
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gb_est1:AW491310
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gb_est2:BF120840
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gb_est2:BI404477
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gb_est2:BF308306
                                                  gb_est1:BE482283
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gb_est2:BE910478
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gb_est2:BG700749
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-O=/cgn2_1/USPTO_spool/US09516493/runat_13022002_125122_18425/app_guery.fasta_1.894
-DB=EST -OpMT=fastap -SUFFIX=rsr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -GGAPOP=6.000
-GGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -EGAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -DELDP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=20 -THR SCORE=DCT -THR MAX=100 -THR MIN=0
-ALIGN=15 -MODE=LOCAL -OUTEMT=pIS -NORM=eXt -MINLEN=0
-MAXLEN=200000000 -USER=US09516493_@CGN1_1_4601 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of: US-09-516-493-7 to: EST:*
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2:BG079217
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| BG34882 602598959F1 NIH_MGC_92 |
| BG478000 602522606F1 NIH_MGC_92 |
| BG478000 602522606F1 NIH_MGC_97 |
| BG281777 60240292F1 NIH_MGC_97 |
| BG281777 60240292F1 NIH_MGC_97 |
| BG281777 60240292F1 NIH_MGC_97 |
| BG986059 UI-M-CG0p-beu-g-08-0-U |
| BE986059 UI-M-CG0p-beu-g-03-0-U |
| BG986059 UI-M-CG0p-beu-g-03-0-U |
| BG986058 WII-P-CPD-IDV-g-05-0-U |
| BG986088 MI-P-CPD-IDV-g-05-0-U |
| BG9707107 602570234F1 NIH_MGC_17 |
| BF1402688 MI-P-CP1-IDMX-a-05-0-U |
| BG707107 602570234F1 NIH_MGC_96 |
| AI094911 qa18b03.x1 NCI_CGAP_BI |
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| BH40268407 WI-P-CP1-IDWX-G-04-0-U |
| BH40268407 WI-P-CP1-IDWX-G-04-0-U |
| BH40268407
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AW4 91 310
AF293722
BF207033
BF410069
BF261630
BF774206
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BEASSE
BF401300
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AI394026
AW249090
BBI404477
AI97246
BE282246
BE282246
BE40365123
AW051497
BF103640
BF400621
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                                                                39 UI-R-CA1-bjt-b-09-0-UI

(7) UI-R-CA0-bma-h-12-0-UI

19 601149349F1 NIH_MGC_19

10 UI-R-CA0-bgs-a-11-0-UI

16 283798 MARC 3BOV BOS the
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602707648F1 NTH_MGC_43
601757442F1 NCI_CGAP_M
UI-R-CAO-bhd-e-10-0-UI
                       vt94a06.rl Soares_mamm
                                               168017 BARC 5BOV Bos
                                                                                                                                                                                   zt55h05.s1 Soares ovai
601870114F1 NTH_MGC_1
                                                                                                                                                                                                                                UI-M-BH3-atr-a-01-0-U
273100 MARC 3BOV Bos 1
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gb_est2:BF468631
gb_est1:AW762507
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                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                     61 lyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeu
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Ratio: 4.541
milarity: 86.095
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CGCCGCCTCCTGGTTCGGGGCTGTCGTGACCCTGGGTGCCGCGGGGGGG
                                                                                         ATCCCTAGCCTGCAGCGCGCCGCGCCCCCGCGCCCCGCGCCTGGACGACGC
                                                                                                              IleProSerLeuGlnArgAlaAlaProProAlaProArgLeuAspAspAl
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1 (bases 1 to 932)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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602527373F1 NIH_MGC_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGGC_21
/tissue_type="Choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Sites using the Directionally cloned into EcoRIXhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit 'C+ra+agene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Stratagene) and Superscript 318 c 314 g 194 t
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/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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BF468631 UI-M-BH3-atr-a-01-0
AW762507 ur63f01.yl NCI_CGAP
AL565390 AL565390 LTI_FL013_
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alignment_block:
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LOCUS BG700749
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                 143 alValGlyIieLeuLeuAlaTyrLeuAlaGlyTrpValLeuGluTrpArg 159
                                                                                                                                                                                                                  110 AlaCysGlyValAlaSerLeuValAlaProValTyrIleSerGluIleAl 126
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                                                                                                                    aTyrProAlaValArgGlyLeuLeuGlySerCysValGlnLeuMetValV 143
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                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1274.50
Ratio: 4.809
milarity: 96.014
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10709 row: p column: 04
High quality sequence stop: 789.
Location/Qualifiers
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1 (bases 1 to 830)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Li
271 c 266 g 189 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hippocampus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:4814451"
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LOCUS BI334832
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1 (bases 1 to 991)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian (
                                                                                                             EST
                                                                                                                                      mRNA sequence.
BI334832
                                                                                                                                                               BI334832 991 bp mRN
602998959F1 NIH_MGC_12 Homo
                                                                   Eukaryota; Metazoa;
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 Unpublished
                                                                                              human
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Clone
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                                                     Hominidae;
             Collection (MGC)
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                                                                                                                                  SerLeuMetLeuLeuLeuMetCysPheMetProGluThrProArgPheLe
              etPheTyrAlaGluThrIlePheGluGluAlaLysPheLysAspSerSer
                                                                                 eGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValM
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Plate: LLAM11347 row: f column:
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TITLE
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1 (bases 1 to 828)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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CGAGCTTCCTGCTGACTCAGCACAGGCGCCAGGAGGCCATGGCCGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCCCGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGC
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Ratio: 4.766
milarity: 95.816
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/lab_host="DH10B (phage-resistant)"
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Gaps: 4
Percent Identity: 94.142
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105 CGCCGCGTCTTCCTCGCCGCCTTCGCCGCTGCCCTGGGCCCACTCAGCTT

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alignment_block:
US-09-516-493-7 x BG771736
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LOCUS BG771736
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ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits,
CDNA Library Preparation: Michael J.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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BG771736
BG771736.1 GI:14082389
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National Institutes of Health, Mammalian
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                       1091.50
4.419
94.636
                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgag ): Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
                                                                                                                                                                                                                                                                                            Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." 319 c 296 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: testis; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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/clone_lib="NIH_MGC_97"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Brownstein (NHGRI),
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                                                                                          seq_documentation_block: LOCUS BG717034
                                                                                                                                 seq_name:
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                                                                                                                                                            GGTCAAAGGCCGCATG
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                                                                              602689093F1 NIH_MGC_97
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sapiens
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                                                                               Homo
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                                                                               clone IMAGE:4821598
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                                                                                                                                                                                                                                                AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe 67
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Ratio: 4.916
milarity: 98.222
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Plate: LLAM10728 row: i column:
High quality sequence stop: 722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 777)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMM/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
cound through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM1228 row: g column: 23
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/lab_host="phl0B (phage-resistant)"
/note="Organ: skin; Vector: porB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the Laboratory of Gerald M. Rubbin (University of
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EST 26-JUN-2001 clone IMAGE:5020563

Gene Collection (MGC)

be

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alignment_scores:
Quality: 1051.00
Ratio: 4.530
----ilarity: 95.473
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US-09-516-493-7 x BG281777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 heGlyPheAla.LeuGlyTyrSerSerProAlaIleProSerLeuGlnAr 33
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                                                                                                                                                                                                                                                                                                                                  ysValProProSerLeuMetLeuLeuMetCysPheMetProGluThr 182
                                                                                                                                                                                                                                                                                                                                                                                               CCCTTCGTGGCCGGCTTTGCCGTCATCACCGCGGCCCAGGACGTGTGGAT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGTGGACCGCGCCGGGCGCAAGCTGAGCCTCTTGCTGCTGCTCCGTG 365
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                   ProPheIleIleGlyValSer 238
                                                              CTGAGCAGAACTTTCACCTGGGCCTAGTGCGGAGCCCGGATCTA...CAA 811
                                                                                      laGluGlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLys 23!
                                                                                                                                                GCGGTCCCTGTGGGGCTCCGAGCAGGGCTGGGAAGA.CCCCCAATCGGGG
                                                                                                                                                                 uargPheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyA 215
                                                                                                                                                                                                                               ProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaIleAla...Le
                                                                                                                                                                                                                                                                                                               GCGTGCCCCCCTCCTCATGCTGCTTCTCATGTGCTTCATGCCCCGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCTCGGCTCCTGTGCAGCTAATGGTCGTCGTCGGCATCCTCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGTGGCCCCGGTCTACATCTCCGAAATCGNCTACCCAGCAGTCCGGGGG
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90
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3 306 c 282 g 158 t 2 others
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Gaps:
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AUTHORS
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SOURCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                            145
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                                           195
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                                                                                                                                                                                                                               1 ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh
                                                                                                                        laAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGly 50
                                                                                                                                                                                                            CGCCGCGTCTTCCTCGCCGCCTTCGCCCTTGCCCTGGGCCCACTCAGCTT
  AlaValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLe
                                             CCGCGCCCCGGCCCCGCGCCTGGACGACGCCGCCGCCTCCTGGTTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1037.00
Ratio: 4.629
milarity: 74.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1837 row: 1 column: 04
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BIll4765
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602861314F1 NIH_MGC_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI114765.1 GI:14565666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                            to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo.sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:5020563"
//clone_ib="NIH_MGC_17"
//tissue_type="rhabdomyosarcoma"
//tab_host="DH10B (phage-resistant)"
//note="Organ: muscle; vector: pOTB7; Site_1: EcoR1;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
97 a 296 c 252 g 155 t 1 others
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                                                                                                                                                                                                                                                                                            BI114765
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72.757
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Page 8
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seq_documentation_block:
LOCUS BE910478
 SOURCE
            KEYWORDS
                        VERSION
                                   ACCESSION
                                                         DEFINITION
                                                                                                     seq_name: gb_est2:BE910478
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                                                                                                                              TC
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                                                                                                                                                                        AGCTGTGGCGGCTCTCATCATTGGACAGAGCAGGCGGAGGCTGCTCCTGG
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                                                                                                                                                                                                                                                                               AlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLys..
                                                                                                                                                                                                                                                                                                                        heIleIleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsn 249
                                                                                                                                                                                                                                                                                                             TCATCATCGGCGTCTCCCTGATGGCCTTCCAGCAGCTGTCGGGGGTCAAC
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                                                   601501005F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903048 5',
                                            mRNA sequence.
            EST
                    BE910478.1
                                   BE910478
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human
                    GI:10407108
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333 aProValSerAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuA
                                                                                                                                                                                                                                  283 aValAlaalaLeuIleMetAspArgAlaGlyArgArgLeuLeuLeuValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 eIleIleGlyValSerLeuMetAlaPheGlnClnLeuSerGlyValAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 GlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 CATCATCGGTGTCTCCCTGATGGCCTTCCAGCAGCTGTCGGGGGGTCAACG
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                                                               LysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerA1
                                                                                                                                                                                                                                                                                           SerSerLeuAlaSerValValGlyValIleGlnValLeuPheThrAl 283
                                                                                                                                                                                                                                                                                                                                                                             CCGTCATGTTCTATGCAGAGACCATCTTTGAAGAGGCCCAAGTTCAAGGAC
                                           AAGCTGACCCA.GGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGC
                                                                                                                         TGTCAGGTGTGATGGTGTTCAGCACGAGTGCCTTCGGCGCCTACTTC
                                                                                                                                                                                                            TGTGGCGGCTCTCATCATGGACAGAGCAGGCGGAGGCTGCTCCTGGTCT
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Ratio: 4.566
nilarity: 95.378
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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/tissue_type="epithelioid carcinoma"
/tissue_type="epithelioid carcinoma"
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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
291 c 287 g 213 t
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/db_xref="taxon:9606"
/clone="IMAGE:3903048"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE986058 664 bp mRNA EST 05-OCT-
UI-M-CG0p-beu-e-08-0-UI.sl NIH_BMAP_Ret4_S2 Mus musculus
UI-M-CG0p-beu-e-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                 Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                            20892-9643, USA
Tel: 301 443 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 664)
Bonaldo, M.F., Lennor
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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301 443 9890
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                                                                                                       Location/Qualifiers
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PheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGly
                                                                                                                                                                                                          1ProProSerLeuMetLeuLeuMetCysPheMetProGluThrProA 184
                                                                                                                                                                                                                                                                GTGGCAGGCTGGTCCTANAGTGGCGCTGGCTGGCCGTGCTGGGCTGTGT
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                                                   GTTTTCTCCTCACTCAACACCAGTACCAGGAGGCCATGGCTGCCTTGCGC
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with The NIH_BMAP_Ret4_S2 library is a subtracted library.

ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please in the library from which this clone was derived, please
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TAG_SEQ=None found"
a 238 c 207 g 142 t 2 others
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17 eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34
                                                                        ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh 17
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                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GEMETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
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20892-9643, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 621)
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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; The NIH_BMAP_Ret4_S2 library is a subtracted library ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.

TAG_SEG=None found"

135 t 1 others
                                                                                                                                                                                                                                                                                          955.50
4.802
97.073
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-beu-g-03-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
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National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3037 row: C column: 03
                                                                                                                                                                                                                       1 (bases 1 to 595)
Kargul,G.J., Dudekula,D.B., Qian,Y.,
,T.S., Carter,M.G. and Ko,M.S.H.
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13037C03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
13037C03-5', mRNA sequence.
                                                                                                                      Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                           Unpublished (2001)
Other_ESTs: H3037C03-3
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                                                                                                                                                                                                                                                                                                                                                                 246 SerGlyValAsnAlaValMetPheTyrAlaGluThrIlePheGluGluAl 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 eGlyAlaGlu...GlnSerPheHisLeuAlaLeuLeuArgGlnProGlyI 229
296 LeuLeuValleuSerGlyValValMetValPheSerThrSerAlaPh
                                                                                                                                                                                                            215 CAAGTTCAAGGACAGCCTGGCCTCGGTCACTGTGGGCATAATCCAGG
                                                                                                                                                                                                                                           262 aLysPheLysAspSerSerLeuAlaSerValValValG1yValI1leG1nV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 leTyrLysProPheIleIleGlyValSerLeuMetAlaPheGlnGlnLeu 245
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                                                                                                                     alLeuPheThrAlaValAlaAlaLeuILeMetAspArgAlaGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTACAAGCCCCTCATCATCGGCATTTCCCTCATGGTCTTCCAGCAGCTG
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                                                                                             TCCTGTTCACTGCTGTGGCGGCCCTCATCATGGACAGAGCAGGCGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, proc. Natl. Acad. Sci. U S A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: psport1; Site_1: Salf; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos ovary cDNA library. Average insert size 1.5 kb. All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source libraries are cloned unidirectionally with Oligo(d)
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libraries"
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/sex="Clones arrayed from a variety of cDNA libraries"
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/clone="H3037C03"
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/strain="C57BL/6J"
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MI-P-CP0-nvv-e-05-0-UI.S1 MI-P-CP0 Sus scrofa cDNA clone
MI-P-CP0-nvv-e-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 Kildee Hall, Ames, IA 50011-3150, Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iowa State University
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                                                                                                             /lab_host="DH10B (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker, Site_1: Not I: Site_2: EcoRI; The MI-P-CPO
library is derived from uterus. For a detailed description
of the library from which this clone was derived, please
visit our web site at http://pigest.genome.iastate.edu/.
The procedure used to create this library has been
                                            TAG_SEQ=None found"
                                                                previously described (Bonaldo, Lennon and Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="MI-P-CPO-nvv-e-05-0-UI"
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                      2 others
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                                                                                                                                                    601890370F1 NIH_MGC_17
         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 920)
                                                                          Homo sapiens
                                                                                                     BF308306.1 GI:11255497
EST.
Unpublished (1999)
                                                                                                                             BF308306
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                                                                                                                                                      Homo
                                                                                                                                                                    mRNA
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                                                                                                                                                     Sapiens cDNA clone IMAGE:4131593
                                                Craniata; Vertebrata;
Catarrhini; Hominidae
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                                                            Euteleostomi;
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alignment_block:
US-09-516-493-7 x BF308306
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                                                                                                                                                                                                           101 LeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eGlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPh
euGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyr 150
                                                                                     lAlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuL
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                                                         .....GTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 308 c 314 g 164 t 1 others
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3.658
65.812
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/clone='IMAGE:4131593"
/clone_iib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
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Gaps: 6
Percent Identity: 61.538
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REFERENCE
AUTHORS
TITLE
JOURNAL
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LOCUS BF140667
                                                                                                                                                                              SOURCE
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                                                                                                                                                                                                               VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1ProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrProA 184
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                                                                                                                                                                                                                                                                                                                  gb_est2:BF140667
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
                                                                                     Amammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 917)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                      BF140667 917 bp mRNA
601786917F1 NCI_CGAP_Lu30 Mui
                                                                                                                                                                  Mus musculus
                                                                                                                                                                             house mouse
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                                                                                                                                Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                       musculus
                                                                                        Mammalian
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   Consortium
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                                                                                                                                     Muridae;
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IMAGE:4014605
   (LLNL)
                                                                                                                                                 Euteleostomi;
                                                                                                                                     Murinae;
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alignment_block:
US-09-516-493-7 x BF140667
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                                     euAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAla
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                                                                                AGGCCTG...GTGCCCATCGCGGCGGAGCCTGTGGATGTCCAAGTGGGAC
                                                                                                                     lAlaIleSerAlaProValSerAlaGlnProValAspAlaSerValGlyL
                                                                                                                                                                  GGTACCTACTTCAAACTGACCCAGAGCCTCCCCAGCAACTCCTCCCACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM9259 row: a column:
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/strain="CZECH II"
/db_xref="taxon:10990"
/clone="IMAGE:4014605"
/clone_lib="WGI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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263 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: No Site_2: SalI; transgenic model wNT-1, expression dr MMTV-LTR enhancer; Cloned unidirectionally. Primer dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 263 c 277 g 214 t
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363		379
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379	uHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuM	396
554		603
396	LysGluPheSerSerLeuMet	408
604	TGGTCTTTTTCTTAAGTTGACCAAAAGAGTTCAAGGCAGCGTCAATGGAA	653
409	PheTrpLeuAlaSerAlaPheCysI	425
654	ACGGGTGGCTTACTGGGTTCCACCGGTTGCG	703
425	425 leheSerValLeuPheThrLeuPhe 433	133
704	TTTCTTGGGCACCTCAAGGTGGTCCCATTTCACACATGGAGCAGTTG	750
434	CysValProGlu.ThrLysGlyLys.ThrLeuGluGlnIleThrAla	448
751	GTCCCTGAGGACTAAAGGCCGGATCTCTGGGACACAGTCTCCACGGC	797
449	HisPheGluGlyArg 453	
798	798 CACTTTCGAGGGAGA 812	

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gb_pr:AB056798
gb_htg:AC017643
gb_htg:AC010025
gb_htg:AC016794
gb_p1:BVU43629
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gb_pat:AX076667
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gb_ro:RNO245935
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                                                                                                     gb_in:AC005974
gb_in:AC007414
gb_in:AE003831
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gb_in:AF199486
gb_htg:AC012854
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9b_htg:AC017247

9b_in:AE003540

9b_htg:AC020266

9b_in:AC011696

9b_in:AC001473

9b_in:AC003825

9b_in:AC008004

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gb_pat:AX179740
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gb_ro:AF232061
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Database length: -341344837
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Database: GenEmbl
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gb_pat:AX076679
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-Q=/cgn2_1/USPTO_spoo1/US09516493/runat_13022002_125123_18437/app_query.fasta_1.
-Q=/cgn2_1/USPTO_spoo1/US09516493/runat_13022002_125123_18437/app_query.fasta_1.
-DB=GenEmb1 -QFMF_fastap -SUFFIX=rege -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09516493_@CGN1_1_7057 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Copyright (c)
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Glutx polypeptide family and nucleic acids Patent: WO 0104145-A 3 18-JAN-2001;
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    Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausan CH-1005, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ibberson,M., Uldry,M. and Thorens,B.
GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
AJ245935
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673 c 580 g 479 t
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741.00
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99.324
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    Identity:
                       Gaps:
    97.973
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US-09-516-493-10 x RNO245935
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LOCUS AB033418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_ro:AB033418
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                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                  JOURNAI
                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGGTGTGGCTACCGGCGTCTGTGTCCTCACCAACTGGTTCATGGCCTT 1297
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Rattus norvegicus glut8
                                                                                                                                                                                                                                          Molecular cloning of a new Published Only in DataBase (bases 1 to 2189)
                                                                                                                                                                                                                                                                                                                                                                                                        glucose transporter 8.
Rattus norvegicus cDNA to mRNA, clone_lib:testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                AB033410
AB033418.1 GI:7592743
                                                                                                                       Submitted (08-OCT-1999) to the DDBJ/EMBL/GenBank databases. Ke Ishibashi, Jichi Medical School, Pharmacology: Minami-kawachi, Tochigi 339-0499, Japan (E-mail:kishiba@jichi.ac.jp, Tel:81-285-58-7326, Fax.81-285-44-5541)
                                                                                                                                                                                                         Direct Submission
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Mammalia; Eutheria; Rodentia;
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    /clone_lib="testis"
109. .1548
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                                                                                                      Location/Qualifiers
                                                                                   .2189
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11-APR-2000

1496

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DEFINITION ACCESSION
                                                       seq_documentation_block:
LOCUS AX076671
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                                                                                                                                               CTGAGCTGGCTTCGGGTTTCAAAAGGAGTGGAGTGGCCTCAG
                                                                                                        gb_pat:AX076671
Sequence 5 from Patent W00104145
AX076671
AX076671.1 GI:12711202
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702 c 609 g 486 t
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                                                                                                                        135 aHisLeuArgAspGlyAspGlyProLeuSerValThrGlySerProGluL
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CCATTTCGAGGGACGATGACAGACCCTTTCTGTGCCTGGGAGCCCCGAGC
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VOLMVVTGIILAYVAGAVLEWRWLAVLGCVPPTLMLLLMCYMPETPFFLLTQHQYOEA
MAALRELMGSEEGWEERPVGAEHQGFOLALLRRPGIYKPLIIGISLMVFOOLSGVNAI
MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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/db_xref="G1:12711203"
/tdb_xref="G1:12711203"
/translation="MSSEDPOETOPLLRPPEARTPRGRRVFLASFAAALGPLNFGFAL
/translation="MSSEDPOETOPLRPPEARTPRGRRVFLASFAAALGPLNFGFAL
GYSSPAIPSLRRTAPPALRLGDNAASWFGAVVTLGAAAGGILGGWLLDRSGRKLSLLL
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                                                        pLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyT 52
                                                                                                                                      LeuValProIleSerAlaGluProAlaAspValHisLeuGlyLeuAlaTr
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Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology
Submitted (02-SEP-1999) Ibberson M.R., Rue du Bugnon 27, Lausann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKnight, R.A., Mueckler, M., Devaskar, S.U. and Moley, K.H. GLUT8 is a glucose transporter responsible for insulin-s glucose uptake in the blastocyst proc. Natl. Acad. Sci. U.S.A. 97 (13), 7313-7318 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moley, K.H., Carayannopoulos, M.O. and Cui, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carayannopoulos, M.O., Chi, M.M., Cui, Y., Pingsterhaus, J.M.,
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1 (bases 1 to 1843)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                  1483.
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                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                       /strain="129"
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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ORIGIN

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                             REFERENCE
                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                      ACCESSION
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                                              AUTHORS
TITLE
                                                                                                                                         AUTHORS
TITLE
                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                       ORGANISM
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1490)

Doege, H., Schurmann, A., Bahrenberg, G., Brauers, A. and Joost, H.G. GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
             Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057
                                                                                           J. Biol. Chem.
20283667
                                              Direct Submission
                                                                                                                                                                                                                                                   glucose transporter 8;
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Aachen,
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                                                           Joost, H.G
                                                                                                                                                                                                                                       house mouse.
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                                                                                                                                          CCATTTCGAGGGACGATGACAGACCCTTTCTGTGCCTGGGAGCCCCGAG
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Sequence 28 from
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/product="glucose transporter 8"
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MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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26. .1459
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26. .1459
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Patent WO0146258
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LOCUS HSA17801
                                                                                                                         seq_name: gb_pr:HSA17801
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                                                                                                                                                                                                                                                         PheValProGluThrLysGlyArgThrLeuGluGlnIleThrAlaHisLe
                                                                                                                                                                                                                                                                                                          TGTGTCCCTGAAACTAAAGGAAAGACTCTGGAACAAATCACAGCCCCATTT 1466
                                                                                                                                                                                                                                                                                                                                                                                                                      lThrLysGluPheAsnSerIleMetGluIleLeuArgProTyrGlyAlaP 104
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                                                                                                                                                                TGAGGGGGGATGACAGCCACTCACT 1491
 glucose transporter
                 Y17801
Y17801.1 GI:7688145
                                                 Homo sapiens mRNA
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Patent: WO 0146258-A 28 28-JUN-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Lal,P., Hillman,J.L., Azimzai,Y., Yue,H.,
Gandhi,A.R., Tang,Y.T. and Khan,F.A.
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1 (bases 1 to 2080)
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AX179740.1 GI:15132104
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/db_xref="taxon:9606"
/note="Incyte ID No: 1416107CB1"
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8; GLUT8 gene
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                                                    (GLUT8 gene)
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alignment_block: US-09-516-493-10 \times HSA17801
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104 heTrpLeuThrAlaAlaPheCysIleLeuSerValLeuPheThrLeuThr 120
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                                                                                                                                                                                                                   37 aValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyP 54
                                                                    lThrLysGluPheAsnSerIleMetGluIleLeuArgProTyrGlyAlaP 104
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                                                                                                                                                        ValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPheLeuVa
                                             GACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with glucose transport activity
J. Biol. Chem. 275 (21), 16275-16280 (2000)
20283667
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MAALRELMGSEGGWEDPFIGAEQSFHLALLROPGIYKFPIIGVSLMAFQQLSGVNAVS
FYAEFITFEBAKFKDSSLASVVVGVLQVLFTAVAALLMDRAGGRELLLVLSGVVWVFFSTS
AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glucose transporter 8"
/protein_id="CAB89809.1"
/db_xref="G1:7684146"
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CSVPFYAGFAVLTAAQDVWMLLGGRLLTGLACGVASLVAPVYLSGIAVEAVTGLLGGGC
CSVPFYAGFAVLTAAQDVWMLLGGRLLTGLACGVASLVAPVYLSGIAVEAVTGLLGGGC
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/db_xref="taxon:9606"
/tissue_type="testis"
27. .1460
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27. .1460
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REFERENCE
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LOCUS AF321324
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                                                                                           38
                                                                                                                                            PheValProGluThrLysGlyArgThrLeuGluGlnIleThrAlaHisLe 137
                    leProTrpLeuLeuMetSerGluIlePheProLeuHisIleLysGlyVal
                                                                                                                             GTCTCCATGGAGGCCGCCGATACCAACGTGGGCCTGGCCTGGCCGGT
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                                                                                        lGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProI 55
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Bos taurus glucose transporter 8 (Glut8) mRNA, partial cds AF321324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Augustin, R., Navarrete-Santos, A. and Fischer, B.
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LOCUS HSA245937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues Calbil. Chem. 275 (7), 4607-4612 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-1999) Ibberson M.R.,
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                                          \label{eq:pullweight} $$ PWILLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPEIKGKTLEQITAHFEGR"$
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LOCUS AX076667
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Sequence 1 from Patent WOO104145.
AX076667
                                                                                                                                                                                                                                                                                     Thorens, B., Ibberson, M. and Uldry, M. Glutx polypeptide family and nucleic Glutx polypeptide family and nucleic patent: WO 0104145-A 1 18-JAN-2001;
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                                                                                                                                                                                                                                                                       University of Lausanne (CH)
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                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                  JOURNAL REFERENCE
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                                                                               Young, J.M.
                                                                                                              Unpublished
                                                                                                                                                                     Povey, S.
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seq_name: gb_pr:HSA011372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPheLeuVa
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                                                                                                                                                                                                                                                                                                                                                                                              HSA011372 2487 bp mRNA
Homo saplens mRNA for sugar transporter
AJ011372
AJ011372.2 GI:9843742
Submitted (17-SEP-1998) Young J.N
Unit, University College London,
London, NW1 2HE, UK
Revised by [3]
                                                                                                                                                                                                Cloning of a sugar transporter gene, a G-beta subunit like gene and
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2487)
                                                                                                                                                                                                                                                                                                                                                                          SLC2A6 gene; sugar transporter
                                                                                         Direct Submission
                                                                                                                                                                            three novel genes in human chromosome
                                                                                                                                                                                                                                            Young, J.M., Woodward, K.J., Aziz, S., Burley, M.,
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                        J.M., MRC Human Live....
Ion, Wolfson House, 4 Stephenson
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                                                                                GlyTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHi
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                     laPheLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgPro
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                                                                                                                                                                                                                                                                                                                                              uLeuValProIleSerAlaGluProAlaAspValHisLeuGly...LeuA
                                                         TGCCCGTGGCGTGGCCTCAGGGCTCTGCCTGGCTGGCTCACCG
                                                                                                                                          GGCTGGGGTCCCATCACCTGGCTGCTCATGTCTGAGGTCCTGCCCCTGCG
Direct Submission Submitted (15-AUG-2000) Young J.M., Dept. Molecular Biotechnology, University of Washington, Health Sciences Building, PO BOX 357730, Seattle, WA 98195, USA On Aug 17, 2000 this sequence version replaced qi:6714698. Related genomic sequence: AC001644 (cosmid 250D5).
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TVALLMRLLQOLTGITF PILVYLQSIFISSTAVLLPEXDDAAIVGAVRLLSVLIAALTMD
LAGRKVLLFVSAAIMFAANLTLGLYIHFGPRPLSPNSTAGLESESWGDLAQPLAAPAG
YLTLVPLLATMLFIMGYAVGWGPITWLLMSEVLPLRARGVASGLCVLASMLTAFVLTK
SCLPVVSTFGLQVPFFFFAAICLVSLVFTGCCVPETKGRSLEQIESFFRMGRRSFLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="sugar transporter"
/protein_id="CAB66155.1"
/db_xref="GI:6714699"
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38. .1561
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AVLGNFSFGYALVYTSPVIPALERSLDPDLHLTKSQASWFGSVFTLGAAAGGLSAMIL
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/map="9q34"
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/chromosome="9"
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LOCUS AX076677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 from Patent Ax076677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Lausanne (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutx polypeptide family and nucleic Patent: WO 0104145-A 11 18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thorens, B., Ibberson, M. and Uldry, M.
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                      209
                    a
  968...970
968...970
/note="Xaa at aa 320 is any one of 536 c 482 g 311 t 3
                                                             /note="Xaa at aa
968. .970
                                                                                                    461. .463
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611. .613
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                                                                                                                                                                                                 460.
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                                                                                                                                                                      /note="Wherein n is any one of a
                                                                                                                                                                                                                 SFLPVVSTFGLQVPFLFFAAICLVSLVFTGCCVPETKGRSLEQIESFFRTGRRSFLR"
                                                                                                                                                                                                                                                            TVALLMRLLQQLTGITPILVYLQSIFDSTAVLLPPKDDAAIVGXVRLLSVLIAALTMD
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                                           Thr or Ala"
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alignment_scores:

Quality:

Ratio:

285.00 2.689 73.103

Percent Identity: 48.966

Gaps:

Percent Similarity:

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MEDLINE
REFERENCE
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SOURCE
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US-09-516-493-10 x AX076677
                                                                  FEATURES
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                                                                                                                                                   TITLE
                                                                                                                                                                           AUTHORS
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                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGTGCCTTTCCTCTTCGCGGCCATCTGCCTGGTGAGCCTGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGlyAlaPheTrpLeuThr.AlaAlaPheCysIleLeuSerValLeuP 117
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1580)
                                                                                   Submitted (16-JUL-1998) H. Joost, Institu
Toxicology, Technical University Aachen,
Aachen, FRG
                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                              Activity and genomic organization of human glucose transporter (GLUT9), a novel member of the family of sugar-transport facilitators predominantly expressed in brain and leucocytes backens. J. 350 Pt 3, 771-776 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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/organism="Homo sapiens"
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                                                               Location/Qualifiers
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for facilitative glucose transporter
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                                                                                                     Institute of Pharmacology and
Nachen, Wendlingweg 2, D-52057
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orter 6, GLUT6
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                                                                                                                                                                                  CCAGGTGCCTTTCTTCTTCGCGGCCATCTGCTTGGTGAGCCTGGTGT
                                                                                                                                                                                                                                                                          CCTTCGTCCTCACCAAGTCCTTCCTGCCAGTGGT.GAGCACCTTCGGCCT
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                                        ThrAlaHisLeuArgAsp.GlyAspGlyPro 143
                                                                                        TCACAGGCTGCTGTGTGCCCGAGACCAAGGGACGGTCCCTGGAGCAGATC
                                                                                                               heThrLeuThrPheValProGluThrLysGlyArgThrLeuGluGlnIle 133
                                                                                                                                                                                                                             TyrGlyAlaPheTrpLeuThr.AlaAlaPheCysIleLeuSerValLeuP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGGGGTCCCATCACCTGGCTGCTCATGTCTGAGGTCCTGCCCCTGCG
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47..1570
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2.689
73.103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPGVRGALGATPQLMAVFGSLSLYALGLLLPWRWLAVAGEAPVLIMILLLSFMPNSP
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                                        glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                           hyperglycaemia, hy neurodegenerative for rat GLUTX1.
                                                                                                                 The present invention re AAB66932-AAB66941). The
                                                                                                                                                                                                                       Nucleic acids encoding
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sport disorder; ischaemia; diabetes; hyperglycaemia;
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Α;
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           Claim
                                 Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disorders; ischemia and diabetes.
                                                                                     P-PSDB;
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13-JUL-2000;
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DB; AAB66934.
           3; Page
                                                                                                                                                                                                                                                                                                                                    ; GLUTX; gene therapy; vaccine; hexose transport modulator; transport disorder; ischaemia; diabetes; hyperglycaemia; ss; ycaemia; glucose metabolism disorder; neurodegenerative disease.
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Human; transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;

Human

transporter and ion channel-1 (TRICH-1)

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disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms Pick's disease, Huntington's disease, and Parkinson's diseases, demyelinating diseases, mental disorder; including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anamemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000;
02-FEB-2000;
10-FEB-2000;
                                                                                                                              syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocardits; Grave's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorders including Alzheimer's disease, amnesia, bipolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is transporter and ion channel-1 (TRICH-1) cDNA TRICH is used as vaccine. TRICH is useful for treating a disease or condition
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  Sequence 2080
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21-JAN-2000;
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                                                                              infections.
                                                                                                             psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duchenne muscular dystrophy, angina and hypertension,
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                                                                                                          and viral,
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Azimzai Y,
                                                                                 TRICH DNA
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2000US-0179758
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Quality:

Length:

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seq_documentation_block:
ID AAF55865 standard;
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                                                                                                                                                                                                                                                                                        Human: GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative di
WPI; 2001-112615/12
                            Thorens B,
                                                                                                      27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                         Human
                                                        (UYLA-) UNIV LAUSANNE
                                                                                                                                      14-JUL-1999;
                                                                                                                                                                     14-JUL-2000; 2000WO-IB01042
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                                                                                                                                                                                                                                                             Homo sapiens
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DE Human secreted protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 70-71; 124pp; English.
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                      Human secreted protein gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disease. The present sequence is the coding sequence
for human GLUTX1.
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                                                                                                                                        AAC80569 standard; cDNA; 1577
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                                                                                                                                                                                                                                         TGAGGGGCGATGACAGCCACTC 1790
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alignment_scores:

Sequence 1577

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352 A;

496 C;

445 G;

284 Ŧ.

0 other;

alignment_block:

Percent Similarity:

Quality: Ratio:

287.50 2.457 68.824

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Identity: 44.706

US-09-516-493-10 x AAC80569

Align seg 1/1

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AAC80569

from:

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to: 1577

174 AGGCCTCTGAGCCCCAAC

ArgProLeu***Asn***TrpIleProArgAlaAlaGlyIleArgHisGl

18

.AGCACTGCGGGCCTGGAAAGCGA 214

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Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opthalmalogical; autoimmune disease; hyperprol cardiovascular disorder; cerebrovascular disorder nervous system disorder; aging; chemotaxis; ss
                                                                                                                                                                                                                                                                                                                                                                                         of their activities include immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers –
                                                                                                                                     system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can
                                                                                                                                                                                                                                                                                                  e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, \,
                                                                                                                                                                                                                                                                                                                                                diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                    fungicide; and opthalmalogical. The secreted proteins, polynucleotides antagonists and agonists may be useful in treating, preventing and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted proteins AAB45120-B45169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide sequences AAC80531-C80580 represent cDNA encoding human
secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 371-372; 440pp; English.
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17-DEC-1999;
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                                                                                                                    also be
                                              invention
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                                                                 used as a food additive or preservative to increase or decrease capabilities. AAC80522-C80530 and AAB45119 represent sequences the isolation and characterisation of the genes and proteins of
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99US-0172410
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ID AAF55870 standard; cE
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AC AAF55870;
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DT 17-APR-2001 (first e
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DE Human GLUTX3 coding s
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Human; GLUTX; gene th
KW hexose transport disc
KW hypoglycaemia; glucos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUTT-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention a treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for human GLUTX3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1541 BP; 209 A;
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Reinhard
                                                                                                                                                                                                                                                                                                                   antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and the product are producted and for detection of transcription levels.
                                                                                                                                                                                                                                                                                                                                                                                  blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                     Sequence 378
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02-JUL-1999;
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                                        uMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyValC
                                                                                                                      LeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLe
              ysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAsn
2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                             gene products are used as genetic or biochemical markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
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                                                                                                                                                     to:
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Randazzo F,
R, Drmanac S,
rcia V, Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide,
                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                     AAF67134
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99US-0142311
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                                                                                                                                                                                                                      281.00
3.306
82.524
                                                                                                                                                                                                                                                                                                     45 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; cancer detection; ss
                                                                                                                                                                                                                                                                                                     130
                                                                                                                                                     from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innis MA, Garcia PD,
Kennedy GC, Pot D, La
Dickson M, Labat I,
LW, Strache-Crain B;
                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                     Ç;
 SEQ ID
                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                    Length: 103
Gaps: 2
Identity: 59.223
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                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J, Kassam
Drmanac R;
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seq_documentation_block:
ID AAA23461 standard;
XX
   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA2346;
The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; cancer; tumour; cardiovascular disorblood disorder; haemophilla; autoimmune disease; diabetes; in infection; fungal; bacterial; viral; HIV; allergy; arthritis;
                                                                                                    New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune
                                                                                                                                        P-PSDB; AAY95019.
                                                                                                                                                                                                   (ALPH-)
                                                                                                                                                                                                                                        23-DEC-1998;
23-DEC-1998;
                                                                                                                                                                                                                                                                 28-SEP-1998;
25-NOV-1998;
                                                                                                                                                                                                                                                                                           09-SEP-1998
                                                                                                                                                                                                                                                                                                    24-AUG-1998;
24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330
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                                                                                                                                                                             Valenzuela
                                                                                                                                                                                                                              23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                         24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                        WO200011015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2000 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                   2000-224657/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                    ALPHAGENE INC
                                                                                                   for treating neurodegenerative
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98US-0102092.
98US-0109978.
                                                                                                                                                                             Yuan
                                                                                                                                                                                                                                        98US-0113645.
98US-0113646.
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98US-0097659.
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                                                                                                                                                                             Hoffman
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                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein vq1_1,
                                                                                                                                                                             Ή,
                                                                                                                                                                             Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                              protein vq1_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                            Rapiejko
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seq_documentation_block:
ID AAF55871 standard; ct
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AC AAF55871;
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DT 17-APR-2001 (first &
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DE Rat GLUTX3 coding sec
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US-09-516-493-10 x AAA23461
                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAA23461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regime. Diseases or conditions that may be treated using the proteins nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention may exhibit one or more activities selected from the fo cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haematon thrombolytic activity; anti-inflammatory activity; and tumour and thrombolytic activity; anti-inflammatory activity; and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic primers and probes. The present sequence represents cDNA encoding one of the 40 proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
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                                                                                                                                                                                                                                                                                                                                                356
                                                                                                                                                                                                                                                                                                                                                                                                          142 lyPro 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 LysGlyArgThrLeuGluGlnIleThrAlaHisLeuArgAsp.GlyAspG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 CATGTCTGAGGTCCTGCCCTGCGTGCCCGTGGCGTGGCCTCAGGGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 uMetSerGluflePheProLeuHisIleLysGlyValAlaThrGlyValC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCTGCTTGGTGAGCCTGGTGTTCACAGGCTGCTGTGTGCCCGAGACC
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                                                             (first entry)
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Percent Identity: 59.223
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alignment_block:
US-09-516-493-10 x AAF55871
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27-AUG-1999; 99US-0151140.
23-FEB-2000; 2000US-0184285.
                                                                                                                          1169
                                                                                                                                                                                          1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 82-83; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. ischemia and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2011 BP; 337 A; 621 C; 593 G; 459 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB66938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyperglycaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding GLUTX glucose transporter proteins, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYLA-) UNIV LAUSANNE
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                GCCCCTGCGTGCCCCTGGTGTGGCCTCAGGGCTCTGCGTGCTGGTCAGCT 1318
                                                                           PheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGluIlePh
                                                                                                                          ACTATCTCACCCTGATACCCCTGCTGCCCACCATGCTCTTCATTATGGGC
                                                                                                                                                                                                                                                      GGGCTGTATGTCCAGCTTGTGCCAAGGACTCTGACCCCCAACAGCACTGT 1118
                                                                                                                                                                                                                                                                                    GlyIleArgHisGluLeuValProIleSerAlaGluProAlaAsp....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat GLUTX3.
                                                                                                                                                                                        GGAGATCGTGACGCTTGGGGGCACGGAGCAGCCCCCAGCCGCGCCCTTCA 1168
                                                                                                                                                       ....LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGly 47
                                                                                                                                                                                                                   .....ValHisLeuGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-112615/12
                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
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                                                                tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
                                         cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
                                                                                                                                                                                                                        sequence tags (sESTs),
                                                                                                                                                                                                                                                                                                                              Claim 1; Page 586; 803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins, comprising secreted
expressed sequence tags (sESTs), useful for treating various disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; chicken; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted expressed sequence tag SEQ ID NO:1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA44914 standard; cDNA; 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGlnIleThrAla.....HisLeuArg 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCAGATCGAGGCCTTCTTCCACACTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuArgProTyrGlyAlaPheTrpLeuThr.AlaAlaPheCysIleLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTCACAGCCTTCGTCCTCACTAAGTACTTCCT.GCTGGCAGTGAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; depression; psoriasis; ss.
                                                                                                                                                                                                                    to AAA45925 represent specifically claimed secreted tags (SESTs), isolated from human, mouse, chicken as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCoy JM,
Treacy M,
   vulnerary; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0104436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LaVallie ER,
, Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins-Racie LA,
   osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the averaging of the ABA45931 represent linker variants which are given
                                             147
                                                                                          108
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                                          ThrGlySerProGluLeuSerTrp
                                                                                                                                luGlnIleThrAlaHisLeuArgAspGly...AspGlyProLeuSerVal 146
                                                                                                                                                                                                                                                                                                                                                                                          laPheLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgPro 100
                                                                                                                                                                                                                          rValLeuPheThrLeuThrPheValProGluThrLysGlyArgThrLeuG
                                                                                                                                                                                                                                                                          GGCTCCACCAGCACCGCGTTCGTGCAGTCAGCCGAGAAGCACTTTCTAAA
                                                                                                                                                                                                                                                                                                                  TyrGly......AlaPheTrpLeuThrAlaAlaPheCysIleLeuSe 114
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                                                                                       .....ACATGCAGCCTGAGCCCCACCATGCCTGGGCCACTGGCCATC
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Quality:
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                                                                                                                                                                 Percent Similarity:
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14-0CT- 14-0CT-	13-OCT- 14-OCT-	13-OCT-	08-OCT-	06-OCT-	04-0CT-	28-SEP- 29-SEP-	23-SEP- 24-SEP-	22-SEP-	16-SEP-	13-SEP-	10-SEP-	01-SEP-	30-AUG-	27-AUG-	27 - AUG - 27 - AUG -	25-AUG- 26-AUG-	R 23-AUG-	R 20-AUG-	R 20-AUG- R 20-AUG-	R 18-AUG-	R 16-AUG-	R 13-AUG-	R 11-AUG-	R 09-AUG- R 10-AUG-	R 09-AUG-	R 06-AUG-	R 05-AUG- R 05-AUG-	R 04-AUG-	R 03-AUG- R 04-AUG-	R 02-AUG-	R 02-AUG-	R 28-JUL-	R 27-JUL-	R 27-JUL-	R 23-JUL-	R 23-JUL-	R 22-JUL-	R 22-JUL-	R 22-JUL-
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alignment_block:
US-09-516-493-10 x AAC36319
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Quality:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                           1265 CACGAAGCAGTCCCAGTC.....
                                             1523
                                                                                          1473 CTTACGGAACTTTCCTCATTTACGCTGCCATCAACGCGCTGGCCATTGTC 1522
                                                                                                                                      1426 AGCGTGGGCTGTTTCTTACACTTTCAACTTCCTCATGTCC...TGGAGCT 1472
                                                                                                                                                                                      1376
                                                                                                                                                                                                                                  1326 CAGGAATGCGAGCAATGCCGTGGGTGGTCATGTCTGAGATATTTCCCCATA 1375
                                                                                                                                                                                                                                                                                 1283 .....CTGGCTGTTGTTGGTATAATGGTGTACATAGGATCGTTTTCAG 1325
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1573 CCAAGCT 1579
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                                                                    117
                                                                                                      17 HisGluLeuValProIleSerAlaGluProAlaAspValHisLeuGlyLe
                                                                                                                                                                                                67 HisIleLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheme 83 :::||||||||||||
                                                                                                                                                                                                                                                33 uAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaV 50
                    eThrAla 135
                                          AACATAAAAGGAGTAGCAGGAGGCATGGCGACGCTGGTGAACTGGTTTGG 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0160741

99US-0160767

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99US-0160814

99US-0160980

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Gaps: 2
Percent Identity: 44.538
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-060-208-1 101.
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-424-406-6 + 97.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-668-128B-7 + 96.
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Query: US-09-516-493-10
                                                       /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-472-934-11 + 
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-323-460A-3 + 
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-461-145C-3 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 351203
Database length: 113238999
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                                                                                                                                                        /cgn2_6/ptcodata/2/ina/PCTUS_COMB.seq:PCT-US91-09160-20
/cgn2_6/ptcodata/2/ina/B_COMB.seq:US-09-043-937A-1 +
/cgn2_6/ptcodata/2/ina/5B_COMB.seq:US-08-533-669A-5 +
/cgn2_6/ptcodata/2/ina/5A_COMB.seq:US-08-472-934-3 + 8
                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-075-533-20 + /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-948-176-20 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence Strd Orig 2Score EScore Len
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-591-025-8 +
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-928-692-9 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-719 -
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-Q=/cgn2_1/USPTO_spool/US99516493/runat_13022002_125123_18457/app_query.fasta_1.894
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09516493_@CGN1_1_97 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of: US-09-516-493-10 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
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96.00 173.13 0.0541
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93.00 170.98 0.0713
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88.50 162.02 0.2250
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LENGTH: 2592
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147 rGlySerProGluLeuSerTrpLeu.......
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-17 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-17 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-4 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-15 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-566-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-675-66-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-675-66-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-675-66-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-675-66-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-675-66-2 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-66-10 - /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-675-66-10 - 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bogan, Jonathan S. APPLICANT: Lodish, Harvey F. TITLE OF INVENTION: Method of TITLE OF INVENTION: Targeting FILE REFERENCE: 0399.1210-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 0399.1210-004
CURRENT APPLICATION NUMBER: US/09/591,025
CURRENT FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1503 GATTGGCCCTGGCCCCATTCCTTGGTTCATCGTGGCCGAGCTCTTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1453 ATGAGCTACGTCTCCATTGTGGCCATCTTTGGCTTCGTGGCATTTTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1603 AGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTATGGG 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1553 AGGGACCCCGCCCGCCAGCCATGGCTGTGGCTGGTTTCTCCAACTGGACG
                                                                                                                                                                                                                                                                                                                                                                                              1653 GCCCTAC...GTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCA 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 aValGlyTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAl 49
                                                                                                                                                                                                                                             IleThrAlaHisLeuArgAspGlyAspGlyProLeu....SerValTh
ATCTCGGCTGCCTTCCACCGGACACCCTCTCTTTTAGAGCAGGAGGTGAA
                                                                                                                                                                                               TCTTCACCTTCTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gProTyrGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValL 116
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Gaps: 3
Percent Identity: 31.081
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-928-692-9
                                                                                                                                                                                                               Align seg 1/1 to: US-08-928-692-9 from: 1
                                                                                                                                                                                                                                                     US-09-516-493-10 x US-08-928-692-9
                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                         1756
                                                                                                                                   1706 ATCTACTTCAACCTGAAAGCCTTATCCGCCATAGCAGTTCTACTTTTCGT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1800 ACCCAGCACAGAACTTGAGTATTTAGGGCCCAGATGAGAATGACCCGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lamsa, Micha
APPLICANT: Hansen, Kim
62 luIlePheProLeuHisIleLysGlyValAlaThrGlyValCysValLeu 78
                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                     29 ValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIl 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                         TGCTTCTTTCGCCGCCGGTCTAGGCCCAGTCCCCTTCATTTAGCCTCTG
                                                                                           eAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10174
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Lamsa, Michael
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                                                                                                                                                                                                                                                                                                           Percent Identity:
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alignment_block:
US-09-516-493-10 x US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D
                                                                                                                                                                                                        3718284TCGGCTCGCTGGTCTGGGTGTACGCCGGGAGAGCTTCCCGTCCCGGCTG
                                                                                                                                                                                                                                                                                                                  3718235.TTGGGGTTCGCCGGCGTGCTGCTGTTCATCGGGTTCAACTTCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                    3718187CTGATCACCGTATTCGCCAACGACTCCGATGGTGGCACGGGGCTGGTG...
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APPLICANT:
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3718381CGCGATCGTTGCCGCCTTCTCGCTCACCATGCTGCGTGTGCTCGGCGGCG 3718430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 LeuValProIleSerAlaGluProAlaAspValHisLeuGlyLeuAlaTr 35
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                                           85 eLeuValThrLysGluPheAsn...SerIleMetGluIleLeuArgProT 101
                                                                                                                                                  69 LysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPh
                                                                                                                                                                                                                                                            52 rpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisIle
                                                                                                                                                                                                                                                                                                                                                                 35 pLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGTCTCCTCGGAAGTTTCATCTACTGGTGGGTGCCGGAGACCAAGGGG 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAsnSerIleMe 95
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1.713
65.414
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alignment_block:
US-09-516-493-10 x US-08-998-416-719/rev
                                                                                                                alignment_scores:
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                                                                                                                                                                        US-08-998-416-719
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                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 719, Application US/08998416 Patent No. 6239264
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                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ĞENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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COUNTRY: U.
27709
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                              Quality:
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Research Triangle Park
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Knechtle, Philipp
Rebischung, Corinne
Rebischung, Corinne
Rebischung, Corinne
Ona SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pohlmann, Rainer
Steiner, Sabine
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                                                         Percent Identity:
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                                                         33.010
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seq_documentation_block:
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                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
REGISTRATION NUMBER: 35,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tartaglia, Louis A. APPLICANT: Weng, Xun
                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 TGCCTCTACATTTTTCTTCTTTGCAACTACCTGGGCCCCCAATTGCGTATG
MOLECULE TYPE:
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STREET: Δ...
STREET: Δ...
STREET: Δ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ThrLysGlyArgThrLeuGluGlnIleThrAlaHisLeuArgAspGlyAs 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 laAlaPheCyslleLeuSerValLeuPheThrLeuThrPheValProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 ACCATACATTACCAATGCGATCAGGTTTTACTACGGCTACGTGTTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly 74
                                                                                                                                                                   TELEPHONE: 61//542-8906
                                                                      TYPE:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                          TOPOLOGY:
                                                STRANDEDNESS:
                                                                                                                                                                 TELEX:
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                                                                                            LENGTH:
                                                                    nucleic acid
                                                                                                                                                                 20015
                                                                                          2343 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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                                                                                                                                                                                                               617/542-5070
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                                              single
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US-09-031-392-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-516-493-10 x US-09-031-392-1
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09299549 Patent No. 6136547
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1606 CAGGCATTTTCCAAAAAGGAACAAAGCATACCCACCAGAAGAGAAAATCGA 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1409 AGCGGCCGGCTGCCTTCATCATTGCAGGCACCGTCAACTGGCTCTCCAAC 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1359 GCCAGGTGGCATCCCGTTCATCTTGACTGGTGAGTTCTTCCAGCAATCTC 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1309 TACCTGAGTATCGTGGGCATTCTGGCCATCATCGCCTCTTTCTGCAGTGG 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 hrLeuThrPheValProGluThrLysGlyArgThrLeu............
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                      APPLICANT: Tartaglia, Louis A.

APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES I
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 rAlaHisLeuArgAspGlyAspGlyProLeuSerValThrGlySerProG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 rGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValLeuPheT 118
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 luLeuSerTrpLeuArgValSer 158
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 leLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAla 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 TrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGl
                                                                                               ZIP:
                                                                                                                                                                     STREET: 225 | CITY: Boston
                                                                                                                                                                       ADDRESSEE: Fisn & NATURE STREET: 225 Franklin Street
OPERATING SYSTEM: Windows 95
                       COMPUTER:
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C...TGTTTCCTAGTCTTTGCTACAATTTGTATCACAGGTGCTATCTACC 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAGCTGTCACTGATGCTCCTGCTTCTTCTCCTTTCACT...ACTCCGA 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTATTTTGTGCTGCCTGAGACCAAAAACAGAACCTATGCAGAAATCAGC 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGCTGTTGGGCTCCTCTTCCCATTCAGTTCAGAAAAGTCTGGACACCTA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgProTy 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACAGCCTGGATTCAAGCTGCC 1725
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Ratio:
                                                                                               02110-2804
                                                                                                                                                MA
                                                                                                                         USA
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                                                                                                                                                                                                                      Fish & Richardson P.C
                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118.50
1.519
55.319
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                                                                                                                                                                                                                                                                                                                        NUCLEIC ACID MOLECULES ENCODING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.532
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; NAME/KEY:
; LOCATION:
US-09-299-549-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-299-549-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           1556
                                                                                                                                                                                                                                                                                                                 1509
                                                                                                                                                                                                                                                                                                                                                                                                        1459 TITGCTGTTGGGCTCCTCTTCCCATTCATTCAGAAAAGTCTGGACACCTA 1508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR AFFLUCTION NUMBER: 09/U31/U2-APPLICATION NUMBER: 09/U31/U2-FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION: Anita
NAME: Meiklejohn, Ph.D., Anita
NAME: Meiklejohn, Ph.D., Anita
NAME: Meiklejohn, Ph.D., Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/299,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2343 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
151 luLeuSerTrpLeuArgValSer 158
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TELEFAX: от.,
Tex: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 TrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGl 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGGCCGGCTGCCTTCATCATTGCAGGCACCGTCAACTGGCTCTCCAAC 1458
                                                                                                                                                                                                                                                                                                                                                        rGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValLeuPheT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAGGTGGCATCCCGTTCATCTTGACTGGTGAGTTCTTCCAGCAATCTC 1408
                                                                                   rAlaHisLeuArgAspGlyAspGlyProLeuSerValThrGlySerProG 151
                                                                                                                                 CAGGCATTTTCCAAAAGGAACAAAGCATACCCACCAGAAGAGAAAATCGA 1655
                                                                                                                                                                                                                                                                                                                 C...TGTTTCCTAGTCTTTGCTACAATTTGTATCACAGGTGCTATCTACC 1555
                                              CTCAGCTGTCACTGATGCTCCTGCTTCTTCTCCTTTCACT...ACTCCGA 1702
                                                                                                                                                                    TGTATTTTGTGCTGCCTGAGACCAAAAACAGAACCTATGCAGAAATCAGC 1605
                                                                                                                                                                                                                                                                  hrLeuThrPheValProGluThrLysGlyArgThrLeu............ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                           PheLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgProTy 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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26-APR-1999
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1.519
55.319
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-730-771-1

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-730-771-1
                                                                                                                                                                                                                                                      alignment_block:
US-09-516-493-10 x US-08-730-771-1
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                                                                                                                                                                                                                   Align seg 1/1 to: US-08-730-771-1 from: 1 to: 2775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2775 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50380
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marshall, Lisa
APPLICANT: Roshak, Amy
TITLE OF INVENTION: A NOVEL HUMAN B-CELL SURFACE MOLECULE
   140
                                                                   HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                         33 euAlaTrpLeuAlaValGlySerMetCysLeuPhelleAlaGlyPheAla 49
                                                                                                       17 sGluLeuValProIleSerAlaGlu...ProAlaAspValHisLeuGlyL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PΑ
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1.217
47.159
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                                                                                                                                                                                                                                                                                                         Gaps: 10
Percent Identity: 27.273
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	; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2775 base pairs	
	TELEFAX: 610-407-0701 TELEX: 846169	
	TELECOMMUNICATION INFOR	
	REFERENCE/DOCKET NUMBER: P	
	ATTORNEY/AGENT INFORMATION: NAME: Prestia, Paul F.	
	FILING DATE:	
	PRIOR APPLICATION NII	
	FILING DATE: APRIL 15, CLASSIFICATION:	
	APPLICATION NUMBER: US/09/	
	SOFTWARE: FastSEQ	
	COMPUTER: IBM Compat	
	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette	
	COUNTR ZIP:	
	STATE: PA	
	STREET: P.O. Box 980	
	CORRESPONDENCE A	
	NUMBER OF SEQUENCES:	
	APPLICANT: MdrSidil, Lisa APPLICANT: Roshak, Amy	
	GENERAL INFORMATION:	
	menta ce 1,	
	<pre>seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-060-208-1</pre>	
	146 lThrGlySerProGluLeu.SerTrp 154 :     :::    :::	
462	CTTTTCAAAGCCATCATCAATTAAGCACAC	
146	.euGluGlnIleThrAlaH :::::::::	
412	AATCTTACCTTTTTGGATTTAACTA	
129	115 alLeuPheThrLeuThrPheValProGluThrLySGlyArgThr	
362	313 GGAATTCAGCTTTAATTTTTTGCCTACAATTCACAATAGAACCTTCAGCA	
115	.laPheCysIleLeu	
312	263 TTAGGTCTCAGTGAAATCCCTGACACTCTACCAAACACAACAGAATTTTT	
106	93SerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLe	
262	216 AGATGTGCATTGAGAAAGAAGCCAACAAAACATATAACTGTGAAAAT	
92	83 etAlaPheLeuValThrLysGluPheAsn	
215	CCTCCT	
83	aThrGlyValCysValLeuThrAs	
178	167rgggTgGTgCTG	
66	euLeu	

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-09-060-208-1
                                                                                                      seq_documentation_block:
                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-818-112-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-516-493-10 x US-09-060-208-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                               Sequence 101,
Patent No. 62
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: (HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                     313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 TTAGGTCTCAGTGAAATCCCTGACACTCTACCAAACACAACAGAATTTTT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrpArgProLeu***Asn***TrpIleProArgAlaAlaGlyIleArgHi
                                                                                                                                                                                                                                                                                                                                                      GACTCATGAATCTTACCTTTTTGGATTTAACTAGGTGCCAGATTAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         etAlaPheLeuValThrLysGluPheAsn.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sGluLeuValProIleSerAlaGlu...ProAlaAspValHisLeuGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCA
                                                                                                                                                                                                                                                                                                          LeuGluGlnIleThrAlaHisLeuArgAspGlyAspGlyProLeuSerVa 146
                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAATTCAGCTTTAATTTTTTGCCTACAATTCACAATAGAACCTTCAGCA 362
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                                                                                                                                                                                                              lThrGlySerProGluLeu.SerTrp 154
                                                                                                                                                                                                                                                                                                                                                                                          alLeuPheThrLeuThrPheValProGluThrLysGlyArgThr....
                                                                                                                                                                                       AACTGGAAATCCCCTGATATTCATGG 488
                                                                                                                                                                                                                                                                     ATACATGAAGACACTTTTCAAAGCCATCATCAATTAAGCACACTTGTGTT 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG...ATGTGCATTGAGAAAGAAGCCAACAAAACATATAACTGTGAAAAT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....ATGGCGTTTGACGTCAGCTGCTTCTTT.........
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                                                                  6290969
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                                                                                   Application US/08818112
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1.217
47.159
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Gaps: 10
Percent Identity: 27.273
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEO ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                Patent No.
                                                                                                                                                                Sequence 10, Application US/07968971A Patent No. 5455167
                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  487
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
71.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS NUMBER OF SEQUENCES: 153
                                                                      APPLICANT: Toni A. Voelker APPLICANT: Huw Maelor Davies TITLE OF INVENTION: Medium-C! TITLE OF INVENTION: In Plant:
                                                                                                                                                                                                                                                                             437
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                                  CORRESPONDENCE ADDRESS:
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                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                           17 sGluLeuValProIle 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 13-MAR
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                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                  TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCA 438
                                                                                                                                                                                                                                                                             CGAGATGCGGCCCGTT
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Ratio:
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98104-7092
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E: Calgene, Inc.
1920 Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton, Raymond
Vedvick, Thomas S
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5.105
86.364
                                                                      Medium-Chain
In Plants
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Gaps: 0
Percent Identity: 77.273
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STREET:

Davis

COMPUTER READABLE FORM:

95616

COUNTRY:

USA

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6 SOFTWARE: Microsoft Word 4.0

Macintosh 6.0.7

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seq_documentation_block:
   Sequence 6, Application US/08424406
   Patent No. 5667997
   GENERAL INFORMATION:
                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-424-406-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-968-971A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 10:
                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US92/04332 FILING DATE: 21-MAY-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/824,247
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
FILING DATE: 7-OCT-1991
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APPLICANT:
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APPLICATION NUMBER: 07/704,861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                            TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCA 56
                                                                                                                                                                        CGAGCTTTCTCCC 69
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Ratio:
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Knutzon, Deborah S.
                Davies, Huw Maelor
                                  Voelker, Toni Alois
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5.389
85.714
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Gaps: 0
Percent Identity: 85.714
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seq_documentation_block:
    Sequence 5, Application US/08472934
    Patent No. 5753446
                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-472-934-5
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US-09-516-493-10 x US-08-424-406-6
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                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                    GENERAL INFORMATION:
APPLICANT: JOHNSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Carl J. Schwedler
REGISTION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGI
TELECOMMUNICATION INFORMATION:
APPLICANT: JOHNSON, TITLE OF INVENTION: TITLE OF INVENTION:
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APPLICATION NUMBER: 1
FILING DATE: 30 Octol
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APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29 October, 1993
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                                                                                                                                                                                       57
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OPERATING SYSTEM: Macintosh
SOFTWARE: Micro-
                                                                                                                                                                                                                         17 sGluLeuValPro 21
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STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Donna E. Scherer REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Elizabeth Lassen REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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30 October, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                           97.00
5.389
85.714
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               GARY L.
METHOD AND PRODUCT FOR REGULATING CELL
   RESPONSIVENESS TO EXTERNAL SIGNALS
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Gaps: 0
Percent Identity: 85.714
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NUMBER OF SEQUENCES:

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alignment_block:
US-09-516-493-10 x US-08-472-934-5
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US-08-472-934-5
                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CPI-004DVCP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/USSA,
APPLICATION NUMBER: PCT/USSA,
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr. Esq.
NAME: Giulio A. DeConti, Jr. Esq.
ODT-004D
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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STREET: STREET: Boston
08
                                                               30 TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCA 79
                             17 s...GluLeuValProIleSerAlaGlu......
                                                                                  APPLICATION NUMBER: 08/3
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
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CGAGGAACAGTGGCCGGTCGGAGCGTCTTCTGGACTTCAGGACTCGCAGG 129
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Percent Identity: 46.939
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alignment_block: us-09-516-493-10 \times us-08-323-460A-5
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                                                                                                                                                                                          Align seg 1/1 to: US-08-323-460A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 303/863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 14-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                 17 s...GluLeuValProIleSerAlaGlu....
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                                                                                                                     30 TGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCA 79
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LOCATION:
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                                                                                                                                                     1 TrpArgProLeu***Asn***TrpIleProArgAlaAlaGlyIleArgHi 17
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                                                  CGAGGAACAGTGGCCGGTCGGAGCGTCTTCTGGACTTCAGGACTCGCAGG 129
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nucleic acid
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METHOD AND PRODUCT FOR REGULATING CELL
RESPONSIVENESS TO EXTERNAL SIGNALS
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Gaps: 2
Percent Identity: 46.939
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CGGCCCGGTCGAGTGGCGCCGCCGAGGCCGAGCCTGG 176

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alignment_block:
US-09-516-493-10 x US-08-461-146C-5
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                                Align seg 1/1 to: US-08-461-146C-5
                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400
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APPLICATION NUMBER:
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1 TrpArgProLeu***Asn***TrpIleProArgAlaAlaGlyIleArgHi 17
                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
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Percent Identity: 46.939
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seq_documentation_block:
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US-08-461-145C-5
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-APR-PRIOR APPLICATION DATA:
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                                                                                                     FEATURE:
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FILING DATE: 14-OCT-1994
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alignment_scores:

Quality:

96.00

Length:

26	17 sGluLeuValProIleSerAlaGlu	1 TrpArgProLeu***Asn***TrpIleProArgAlaAlaGlyIleArgHi 17	Align seg 1/1 to: US-08-461-145C-5 from: 1 to: 3089	alignment_block: US-09-516-493-10 x US-08-461-145C-5	Ratio: 3.429 Gaps: 2 Percent Similarity: 57.143 Percent Identity: 46.939
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gb_est2:BG079217
gb_est2:BF206274
gb_gss:AZ985752
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gb_est1:AW310448
gb_est1:AW310827
gb_est2:BG586896
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gb_est1:AW657233
gb_est1:AV555051
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                                  gb_est1:AA627408
gb_est2:R59842
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gb_est1:AW310338
gb_est1:AV526551
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gb_est1:BE020975
gb_est1:AW940244
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gb_est1:AW141319
gb_est1:AI405787
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gb_est2:BF311341
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gb_est2:BF146289
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                                               236 GCTGGCTGTAGGCAGCATGTGCCTCTTCATTGCTGGCTTGGCGGTGGGCT
                                                                    35 pleuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyT
52 rpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisIle
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High quality sequence stop: 644.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10000"
/clone="IMAGE:3986651"
/clone_iib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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IMAGE:3986651
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95396786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp. Rattus sp.
                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712, Medical Center Drive, Rockvi Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H34451.1 GI:979868
EST.
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                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                          For clone availability please contact (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Warmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                   48
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                                                                                                                                                                                                                                                                                                                                    nhlee@tigr.org
      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene" 88 t 1 others
                                                                                                                             /organism="Rattus sp."
/db_xref="ATCC (inhost):2005510"
/db_xref="taxon:10118"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
                                                                                                                                                                                                                                              Location/Qualifiers
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SOURCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GCTGGCTGTAGGCAGCATGTGCCTCTTCATCGCTGGTTTTGCAGTAGGCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 pLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 LeuValProIleSerAlaGluProAlaAspValHisLeuGlyLeuAlaTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGGTGCCCATCTCCGCAGAGCCTGCTGATGTTCACCTGGGGCTGGCCTG
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                                                                                                               High quality sequence stop: 745.
Location/Qualifiers
                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                             http://image.llnl.gov
                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 949)
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BG749509
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/clone="IMAGE:4844411"
/clone_lib="NIH_MGC_43"
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                                                           /organism="Homo sapiens"
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REFERENCE
AUTHORS
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LOCUS BE231636
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                                                                                                                                                                                                                                                                                                                          gb_est1:BE231636
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 546)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., and Keele, J.W.
                                                                                                                                                                                                                            BE231636 546 bp mRNA ES
136437 MARC 1PIG Sus scrofa cDNA 5', mRNA
BE231636
Design and use of two pooled tissue normalized cDNA EST discovery in swine \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Stratagene) and Superscript II RT (Life Technologies)
Note: this is a NIH_MGC Library. |"
a 302 c 264 g 223 t
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4.678
94.400
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Gaps: 0
Percent Identity: 80.000
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                                                                          Smith, T.P.L.,
                                                                                                                Suidae; Sus.
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                    libraries for
                                                      Laegreid, W.W
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BASE COUNT
ORIGIN
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US-09-516-493-10 x BE231636
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                                                                                                                                                                                                                                                    108 laAlaPheCysIleLeuSerValLeuPheThrLeuThrPheValProGlu 124
                                                                                                                                                                                                                                                                                                 202 CAGCAGCCTCATGGAGGTGCTCAGGCCCTACGGTGCCTTCTGGCTCGCCT 251
                                                                                                                                                                                                                                                                                                                                                                                 152 GTCTGTGTCCTCACCAACTGGCTCATGGCCTTTCTGGTGACAAAGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 TCCTCATGTCTGAGATCTTCCCTCTGCACGTCAAGGGCGTGGCCACCGGC
                                                                                                                                                                                                                                                                                                                       91 eAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThrA 108
                                                                                                                                                                                                                                                                                                                                                                                                                           75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                              ThrLysGlyArgThrLeuGluGlnIleThrAlaHis.LeuArgAspGlyA 141
                                                                                                                                                                                                                                                                                                                                                                                                       ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
                                                                             spGlyProLeuSerValThrGlySerProGluLeuSerTrpLeuArgVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCCGCCGATGCCAGCGTGGGGCTGGCCTGGCTGGCGGTGGGCAGCGT
                                          ATGACAGCCTCTCCCCGAGAGTGGCCACCCCTCTTANCTGGACTTGGCTT
                                                                                                                            ACCAAAGGGAAGACTCTGGAGCAGATCACAGCCCATTTTGAGG...GGCG
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
SerLysGlyValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG Plate: 70 row: A column: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Sit
Library made from pooled tissue from day 11,
and 30 embryos."
182 c 162 g 124 t 2 others
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/tissue_type="pooled"
/lab_host="DH10B"
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4.349
90.000
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/db_xref="taxon:9823"
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TGGGCGGAGGGGATAGAG

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alignment_block:
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VERSION
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ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                         577
                                                                                                                                           627
                                                                                                                                                                                                                 677 CGTGGNCANCATGTGCCTCTTTCNATCGCCNGCTTTTGCGGTGGGCTGGG
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                                                                                                 69
                                                                                                                                                      53. lyProIle.ProTrpLeuLeuMetSerGluIlePheProLeu.His.Ile 68
                                                                                                                                                                                                                                                                      37
                                                                                                                                                                                                                                                                                                                         21 ProIleSerAlaGluProAlaAspValHisLeuGlyLeuAlaTrpLeuAl 37
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                                                                                 LysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPh 85
                                                                                                                             GGCCCATCCCCTTGGCTCCTCATGTCAGAGATCTTCCCCCCTCGCACTNTC
\tt eLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgProTyrG
                                                                                                                                                                                                                                            aValGlySerMetCysLeuPheIleAla...GlyPheAlaValGlyTrpG 53
                                              AAGGGCGTGGCGACAGGCATCTGCGTCCNCACCAACTGGCTCATGGCCTT
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --...... gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
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1 (bases 1 to 752)
Li,W.B., Gruber,C.,
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segref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Togan: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468.50
4.110
88.372
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/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Gaps: 4
Percent Identity: 72.868
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alignment_block: US-09-516-493-10 x
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AUTHORS
TITLE
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SOURCE
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VERSION
                                                          Align seg 1/1 to:
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31 LeuGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGl
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                                                                                                                                                                       Quality:
Ratio:
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 712)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM10402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/ILNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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BG290178.1 GI:13046711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG290178 712 bp mRNA EST 21-FEB-2001 602385265F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4514200
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                                                          BG290178
                                                                                               BG290178
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                                                                                                                                                                                                                                                                         /tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: bladder; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 221 c 211 g 163 t
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/clone_lib="NIH_MGC_93"
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  Ratio:
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                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BE910478
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                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM9706 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can
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                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 710.
                                                                                                                                /Clone_lib="NIH_MGC_70"
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/lab_host="DH108 (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Sit Site_2: SalI; Cloned unidirectionally. Primer: Average insert size 1.1 kb. Library constructe Technologies."
291 c 287 g 213 t
464.00
3.742
62.000
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Xiao, H.S., Han, Z.G.,
                                                                                                                                                                                      mRNA sequence.
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Distinct gene expression
                Zhang, X.
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                             Guo, C., Yan, Q.,
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                              Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G.,
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                                      seq_name: gb_est1:AW248655
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                                                                                                                                                                                                                                                CACCTTTGTCCCTTGGACTAAAGGCAGGACTTTGGAACAAATCACAGGCC
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                                                                                                                                                                                                                                                                                                                               GCCTTTTGGCTCAACGGTGTCTTTTGTATTCTTAGCGGCCTTTTCACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGGGGTACCGGGTCTGGGTCCTCACCAACTGGTTCATGGGCTTTC
                                                                                  GAGCTGGCTTCGGGTTTCAAAAGGAGTGGAGTGGCCT 340
                                                                                                                                                                                      is.LeuArgAspGlyAspGlyProLeuSerValThrGlySerProGluLe 152
                                                                                                                                                               ATTTTGAGGGACGGTGACGCACCCTT.TCTGTGACTGGCAACCCTGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induced by peripheral nerve axotomy Unpublished (2001)
Contact: Zhang xu
Laboratory of Sensory System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute of Neuroscience
320 Yue Yang Road, Shangha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYA=No.
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BACKWARD: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: xu.zhang@ion.ac.cn
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: 86-21-64748700-121
: 86-21-64713446
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4.413
92.035
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/dev_stage="adult"
146 c 138 g 136 t
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/db_xref="taxon:10116"
/clone="DRNCFD10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rat DRG Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other BSTS: 2020/07/27-07
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates;
1 (bases 1 to 496)
NIH-MGC h++~ '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM5 row: A column: 16 High quality sequence stop: 415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_ESTs: 2820759.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="Organ: lung: Vector: pOTB): Site_1: XhoI; Site_2:
RCORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 145 c 142 g 92 t 1 others
                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:2820759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Quality: Ratio: 365.00 4.803 97.436 Percent Length: 78
Gaps: 0
Identity: 82.051

Align seg 1/1 to reverse of: AW248655 from: 1 to: 496

- ProlleSerAlaGluProAlaAspValHisLeuGlyLeuAlaTrpLeuAl
- aValGlySerMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyP 54 CGTGGGCAGCATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGGGGGC 368
- rolleProTrpLeuLeuMetSerGlullePheProLeuHisIleLysGly 70

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KEYWORDS
SOURCE
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ORIGIN
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                                                                                                                                                                alignment_scores
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                                      US-09-516-493-10 x BF774206
Align seg 1/1
                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE774206 440 bp mRNA EST 283798 MARC 3BOV BOS taurus cDNA 5', mRNA sequence.
BE774206
BF774206.1 GI:12122106
EST.
                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 83 row: H column: 1
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkruy, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 83 row: H column: 1
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to:
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BF774206
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141 c 135 g 99 t
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                   357.00
5.028
97.260
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
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from:
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440
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LOCUS BF146289
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                                                                           Align seg 1/1 to:
                                                                                                                  US-09-516-493-10 x BF146289
                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 TCCCGTGGCTCCTCATGTCTGAGATCTTCCCTCTGCATGTCAAGGGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 GGGCAGCATGTGCCTCTTCATCGCCGGCTTCGCTGTGGGCTGGGGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 rLysGluPheAsnSerIle 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPheLeuValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
                  58 LeuLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGl
2 CTCCTCATGTCAGAGATCTTCCCGCTGCACGTCAAGGGTGTGGCTACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leProTrpLeuLeuMetSerGluIlePheProLeuHisIleLysGlyVal
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                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST00181 rabbit blastocyst mrNA to cDNA Oryctolagus cuniculus cDNA clone G81 similar to glucose transporter 8 (GLUT8), mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Anatomy and Cell Biology
Martin Luther University Halle-Wittenberg, Medical Faculty
Grosse Steinstrasse 52, D-06097 Halle, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
1 (bases 1 to 235)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: silke.kietz@gmx.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kietz S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression of glucose transporters in rabbit preimplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kietz, S., Augustin, R. and Fischer, B.
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                                                                                                                                                                       351.00
4.680
96.154
                                                                                                                                                                                                                                                                                                              /clone_lib="rabbit blastocyst mRNA to cDNA" /dev_stage="six days old preimplantation embryo" 78\ c 61\ g 57\ t
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryctolagus cuniculus"
/strain="hybrid strain Zika"
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           /clone="G81"
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Gaps: 0
Percent Identity: 84.615
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74 yValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluP

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COMMENT
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LOCUS BF742266
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGCCTTCTGCATCTTCGGCGTCCTTTTCACTTTGTTCTGCGTCCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
BF742266
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RC1-BTN0409-021000-012-e12 BTN0409 Homo sapiens cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF742266.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RC1-BTN0409-021000-012-e12&L3=2000-10-02&t4=1)
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
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                                                                                               /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                /clone_lib="BTN0409"
                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon
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/db_xref="taxon:9606"
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Quality:

348.50

Length:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 CCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGGGCATGGCGCTGCATG
                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisIle
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
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EST.
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plate: LLAM9259 row: a column: 06
High quality sequence stop: 605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 917)
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Mammalia; Eutheria; Rodentia;
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91.667
                 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by mMTV-LFR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" a 263 c 277 g 214 t
                                                                                                                                                                                                       /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4014605"
                                                                                                                                         /tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                    /clone_lib="NCT_CGAP_Lu30"
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; Murinae; Mus
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COMMENT
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LOCUS BG303512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-516-493-10 x BF140667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eLeuValThr....LysGluPheAsnSer 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCTTAAGTTGACCAAAAGAGTTCAAGGCA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGGTGTGGCTACCGGCGTCTGTGTCCTCACCAACTGGTTCATGGTCTT 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostel; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 295)

Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hiller,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU Zebraiish EST Project 1999
                                                                                                                                                                                                                     Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG303512
BG303512.1 GI:13101039
EST.
                                                                                                                                                                                    Seq
                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: S.L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                       Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zebrafish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f156g08.xl Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 3817934\ 3' similar to TR:Q9V610 Q9V610 CG8234 PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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                                                                  /organism="Danio rerio"
/strain="AB"
/clone_lib="Sugano Kawakami zebrafish
                       /clone="3817934"
                                               /db_xref="taxon:7955"
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4.307
97.403
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  COMMENT
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DEFINITION
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US-09-516-493-10 x BG303512/rev
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ORIGIN
                                                                     REFERENCE
                                                                                                                                             SOURCE
                                                                                                                                                          KEYWORDS
                                                                                                                                                                                VERSION
                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS BF311341
                                 AUTHORS
TITLE
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                                                                                                                          ORGANISM
                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAl 49
                                                                                                                                                                                                                                                                                                                                                                              euPheThrLeuThrPheValProGluThrLysGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCGCAGGAACATTTTGGATGTTCTCGGCACTGTGTGCTTCTAATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGCCTTCATTGACACCAAAACCTTCCAGAACCTCATGGATGCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetAlaPheLeuValThrLysGluPheAsnSerIleMetGluIleLeuAr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euHisIleLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPhe 82
                                                                                                                                                                                                                                                                                                                                              TCTTCACGGCTTTCTTTGTCCCCGAGACCAAAGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gProTyrGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTGGTTGGGGTCCTACTCCGTGGCTGGTGATGTCAGAGATCTTCCCCCA
                                                    Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 911)
                                                                                                                                                            EST.
                Unpublished (1999)
                                                                                                                                                                                               mRNA sequence.
BF311341
                                                                                                                                                                                                                               601896741F1 NIH_MGC_19
Contact: Robert Strausberg, Ph.D
                               NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
                                                                                                                                                                              BF311341.1 GI:11259060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insert. Size selection was performed to exclude fragments <al. kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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4.025
82.292
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                                                                                                                                                                                                                                                      911
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Gaps: 0
Percent Identity: 57.292
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                                                                                                                                                                                                                                                      mRNA
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                                   Mammalian
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                                   Gene Collection (MGC)
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FEATURES
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US-09-516-493-10 x BF311341
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAla...ValGlySe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGCCTGTTGACGCCAGCGTGGGCTGGCCTGGGCTGGCCGATGGGCAGA 50
                                                                                                                                                              alThrLysGluPheAsnSerIle...MetGluIleLeuArgProTyrGly 102
                                                                                                                                                                                                                                                                                                                             GCCCAGTTTTCGAGGGGCGAT 371
                                                                                                                                                                                                                                                     TGACCAAGGAGTTCAGGCAGGTCCTCATGGAGGTCCTCAGGCCCTATGGA
                                    AlaHisLeuArgAspGlyAsp 141
                                                                                  TTTGTTCTGTGTCCCTGAAACTAAAGGAAATGACTCTGGAACAAATCACA
                                                                                                      rLeuThrPheValProGluThrLysGlyArg.ThrLeuGluGlnIleThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM1015 row: a column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: POTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
62 a 275 c 267 g 207 t
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2.990
81.890
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/db_xref="taxon:9606"
/clone="IMAGE:4125971"
/clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Gaps: 10
Percent Identity: 62.992
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gb_in:AE003831
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gb_ro:MMU17802
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Database length: -341344837
Search time (sec): 3231.410000
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gb_ro:RNO245935
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-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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AF199486 Drosophila melanogas:
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! AL445222 Human DNA sequence
AX072418 Sequence 2890 from Pat
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AF321324 Bos taurus glucose tr
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AJ245935 Rattus norvegicus mRI
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! AC091762 Mus musculus
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gb_htg:AC019887
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                                                       ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
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Mammalia; Eutheria;
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VOLMVVTGIILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTQHQYQEA
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MFYANTIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRKLLLALSGVIMVFSM
SAFGTYFKLTQSGPSNSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGP
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2.4e-07
2.5e-07
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Sciurognathi; Muridae; Murinae;
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! AC019887 Drosophila melano
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US-09-516-493-12 x RNO245935
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Ratio: 5.404
Percent Similarity: 100.000
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1166 GTGCCTCTTCATCGCTGGTTTTGCAGTAGGCTGGGGACCCATCCCCTGGC
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                                                                                                                  1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe 17
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                                           tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL 34
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GLUTXI, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
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Rattus norvegicus mRNA
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Rattus norvegicus
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/db_xref="taxon:10116"
30. .1466
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MFYANTIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRKLLLALSGVIMVFSM
SAFGTYFKLTQSGPSNSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWGP
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673 c 580 g 479 t
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30. .1466
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1. .2087
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/codon_start=1
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seq_name: gb_ro:AB033418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-OCT-1999) to the DDBJ/EMBL/GenBank databases. Kenichi Ishibashi, Jichi Medical School, Pharmacology; Minami-kawachi, Kawachi, Tochigi 329-0498, Japan (E-mail:kishiba@jichi.ac.jp, Tel:81-285-58-7326, Fax:81-285-44-5541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular cloning of a new Published Only in DataBase 2 (bases 1 to 2189)
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Rattus norvegicus glut8
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MSAFGTYFKLTQSGPSNSSHVGLLVPISAEPADVHLGLAWLAVGSMCLFIAGFAVGWG
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Quality:

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Length:

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Ratio:

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  Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutx polypeptide family and nucleic acids encoding Patent: WO 0104145-A 5 18-JAN-2001; University of Lausanne (CH)
                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
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SAFGTYEKLTQSLPSNSSHVGLVPIAAEPVDVQVGLAWLAVGSWCLFIAGEAVGWGPI
PWLLMSEIFPLHYKGVATGICVLTNWFMAFLVTKEFNSVMEMLRPYGAFWLTAAFCAL
SVLFTLTVVPETKGRTLEQVTAHFEGR*
a 673 c 584 g 464 t
                                                                                                                                                                                                                                                  GYSSPAIPSLRRTAPPALRLGDNÄASWFGAVVTLGAAAGGILGGWLLDRSGRKLSLLLCTVPEVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVOLMVVTGILLAYVAGWVLEWRWLAVLGCVPPTLMLLLMCYMPETPRFLLTOHOYOEA
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482.00
5.183
98.936
                                                                                                                                                                                                                                      MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUTX1, a novel mammalian glucose transporter expressed central nervous system and insulin-sensitive tissues J. Biol. Chem. 275 (7), 4607-4612 (2000)
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MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
                                                                                                                                                                                                                                                                                                                                                                              SWITZERLAND
                                                                                                                                                                                                      /gene="GLUTX1"
                                                                                                                                                                                                                                               /gene="GLUTX1"
                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus mRNA for Y17802
                                                                                                                                               Direct Submission
Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Submitted (16-JUL-1998) H. Joost, Mendlingweg 2, D-52057
                                                                                                                                                                                                                                 Doege, H., Schurmann, A., Bahrenberg, G., Brauers, A. and Joost, H.G. GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity J. Biol. Chem. 275 (21), 16275-16280 (2000)
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glucose transporter 8; GLUT8 gene
                                                                                                                                  Toxicology, Technical University Aachen, Wendlingweg Aachen, FRG
                                                                                                                                                                                              Joost, H.G.
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                                                                                                                                                                                                          (bases 1 to 1490)
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SVLFTLTVVPETKGRTLEQVTAHFEGR"
a 673 c 584 g 464 t
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26. .1459
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26. .1459
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5.183
98.936
/gene="GLUT8"
                                                                                                                   Location/Qualifiers
                                                                                                      .1490
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                                                                                                                                                                                                                                                                                                                                                                                                                      glucose transporter
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Gaps:
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                                                                                                                                    REFERENCE
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TITLE
               AUTHORS
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seq_documentation_block:
LOCUS AF232061
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                                                                                                                                                                           Carayannopoulos,M.O., Chi,M.M., Cui,Y., Pingsterhaus,J.M., McKnight,R.A., Mueckler,M., Devaskar,S.U. and Moley,K.H. GLUT8 is a glucose transporter responsible for insulin-stiglucose uptake in the blastocyst proc. Natl. Acad. Sci. U.S.A. 97 (13), 7313-7318 (2000)
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                 Moley, K.H., Carayannopoulos, M.O. and Cui, Y
                                                                                                                                           20319023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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LOCUS AF321324
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    Quality:
                                                                                            VERSION
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                                         ORGANISM
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                                                                                                                Bos taurus glucose transporter 8 AF321324
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                       Bos taurus
                                                                                              AF321324.1 GI:14582715
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98.936
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PWLLMSEIFPLHVKGVATGICVLTNWFMAFLVTKEFSSVMEMLRPYGAFWLTAAFCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLLALSGVIMVFSM
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MAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLSGVNAI
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CTVPFVTGFAVITAARDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSC
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Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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Gaps: 0
Percent Identity: 90.426
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Pecora;
                                                                                                                                                   02-JUL-2001
Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                        51 ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                34 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL
                                                                                                                                                                                                                               84 laAlaPheCysIleLeuSerValLeuPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe
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                                                                                                                                                                                                                                                                                                                                                  GTCTGCGTCCTCACCAACTGGTTCATGGCCTTTCTGGTGACCAAAGAGTT
                                                                                                                                                                                           CTGCCTTCTGCATCTTCGGTGTCCTTTTCACT 936
                                                                                                                                                     gb_pr:HSA17801
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Ratio:
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1 (bases 1 to 1012)

Augustin,R., Navarrete-Santos,A. and Fischer,B.
Direct Submission
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                                        Y17801.1 GI:7688145
                                                                        Homo sapiens mRNA
human
                  glucose transporter 8;
                                                                                                HSA17801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVAPSEMLLLMCEMPETPRELLSQHKHQEAMAAMQELMGYAQGWEEPPLGAQHQDEHV
AQLRRPGVYKPETIGISLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="glucose transporter 8"
/protein_id="AAK69606.1"
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/db_xref="GI:14582716"
/translation="ISEIAYPEVRGLLGSCVQLMVVTGILLAYLAGWVLEWRWLAVLG
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4.925
98.936
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/db_xref="taxon:9913"
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                                                            bp mRNA rai for glucose transporter 8 (GLUT8 gene).
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Gaps: 0
Percent Identity: 86.170
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                  GLUT8 gene
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                                                                                                                                                                                                                                                                                                         34 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly 50
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                          laAlaPheCysIleLeuSerValLeuPheThr 94
                                                                                                                                                                                                   CAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGCTTGCCT 1359
                                                                                                   eAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThrA 84
                                                                                                                                                                            ATCTGCGTCCTCACCAACTGGCCTCATGGCCTTTCTCGTGACCAAGGAGTT
                                                                                                                                                                                                                                                                            TCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGC 1259
                                                                                                                                                                                                                                                                                                                                                                               GTGCCTCTTCATCGCCGGCTTTGCGGTGGGCCTGGGGCCCATCCCCTGGC 1209
Quality:
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J. Biol. Chem. 275 (21), 16275-16280 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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VQLMVVVGILLAYLAGWVLEWKHLAVLGCVPPSLMLLLTGFMPETPRFLLTQHRAQBA
VQLMVVVGILLAYLAGWVLEWKHLAVLGCVPPSLMLLTGFMPETPRFLLTQHGAAAGGVLGVNAAV
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AFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPI
PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
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27. .1
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27. .1460
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Gaps: 0
Percent Identity: 85.106
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             AJ245937.1 GI:7018305 glucose transporter; Gl
                                                                 Homo sapiens mRNA for glucose transporter (GLUTX1 gene).
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Gandhi,A.R., Tang,Y.T. and Khan,F.A.
Transporters and ion channels
Patent: wo 014658-A 28 28-JUN-2001;
Incyte Genomics, Inc. (US)
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/db_xref="taxon:9606"
/note="Incyte ID No: 1416107CB1"
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MEDLINE
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CCGCTTTCTGCATCTTCAGTGTCCTTTTCACT 1368
                               laAlaPheCysIleLeuSerValLeuPheThr
                                                               CAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGCTTGCCT 1336
                                                                              eAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThrA 84
                                                                                                                            ATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTT 1286
                                                                                                                                                                                         TCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                                                                                                                                                            eAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThrA
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Location/Qualifiers
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/db_xref="G1:12711199"
/db_xref="G1:12711199"
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/trans1ation="mypedphetryphi.gppggsaprgrrvflaafaaalgvldgrklslil
GYSSPAIPSLORAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLIL
GYPSPVAGFAVITAAQDVWMLLGGRLLTGLAGGVASLVAPVY1SEIAVPAVRGLLGSC
VQLMVVVGILLAYLAGWLEBRWLAVLGCVPPSSLMLLMCFWPBETPRFLITDGHROEA
MAALRFLWGSEOGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQOLSGVNAVM
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AFGAVKKLTQGGFGNSSHVALSAPVAAQPVDASVGLAWLAVGNMCLFTAGFAVGWGPI
PWLLMSEIFFD-HVKCVATGLCVLTMVLAMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF
SVLFTLFCVPEIKGKTLEQITAHFEGR"
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/db_xref="taxon:9606"
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seq_documentation_block: LOCUS AL445222 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL445222 225370 bp DNA PRI 24-APR-2001 Human DNA sequence from clone RP11-356B19 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RP11-356B19 The true left end of clone RP11-373J8 is at 96439 in this sequence. The true right end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/HGP/Chr9
RP11-356B19 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISSPROT\colon \mbox{Tr:, TREMBL; } \mbox{Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Apr 26, 2001 this sequence version replaced gi:13277497. During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB10 1SA,
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23455. .23821
/note="Single clone region. Assembly confirmed restriction digest data."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="9"
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35 uMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyValC 52
                                                                                                               19 LeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLe
                                                                                31 CTCTTCATCATGGGCTACGCCGTGGGCTGGGGTCCCATCACCTGGCTGCT 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 378)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057 Aachen, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activity and genomic organization of human glucose transporter (GLUT9), a novel member of the family of sugar-transport facilitators predominantly expressed in brain and leucocytes Biochem. J. 350 Pt 3, 771-776 (2000)
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1455 CCATCTGCTTGGTGAGCCTGGTGTTCACA 1483
                                                                                     1406 CCAGTGGT.GAGCACCTTCGGCCTCCAGGTGCCTTTCTTCTTCGCGG
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                                                                                                                           SerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThr.AlaA
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23-FEB-2000;
13-JUL-2000;
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                         1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe
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                                                                                 The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
                                                                                                                                                                                                          Nucleic acids encoding GLUTX of the prevention, diagnosis and e.g. ischemia and diabetes -
function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypeolycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
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; 2000US-0184285.
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sport disorder; ischaemia; diabetes; hyperglycaemia; ss;
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
glucose carriers GLUTI-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for murine GLUTX1.
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                                                                                                                                                                                                                                                              Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders e.g. ischemia and diabetes -
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                                                                                                                                                   AAB66932-AAB66941).
                                                                                                                                                                                                                Claim 3; Page 73-74; 124pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Thorens B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypoglycaemia; glucose metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine GLUTX1 coding sequence
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                                                                                                                                              present invention relates to GLUTX proteins (AAF55865-AAF55871 and 56932-AAB66941). The GLUTX proteins are related to the facultative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCTTCTGTATCCTCAGCGTCCTTTTCACG
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99US-0151140.
2000US-0184285.
2000US-0616132.
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Sequence 2072 BP;

351 A; 673 C;

584 G;

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23-DEC-1999; 22-DEC-2000;

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2000WO-US35095

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alignment_block:
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ID AAD09552 standard:
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                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                         rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;
                                                             28-JUN-2001
                                                                                              WO200146258-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human transporter and ion channel-1 (TRICH-1) cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                           Location/Qualifiers 46..1479
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                                                                                                                             "Human TRICH-1 protein"
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alignment_block:
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02-FEB-2000;
10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is transporter and ion channel-1 (TRICH-1) cDNA TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including AIDS, adult respiratory distress syndrome (ARDS), allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 140-141; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological
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21-JAN-2000;
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2000US-0181625.
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Yao MG,
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alignment_block:

Percent Similarity:

Percent Identity:

Gaps:

Ratio:

Align seg 1/1 US-09-516-493-12 x

to:

AAF55865 AAF55865

from:

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2217

GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                                         AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and
                                                                       Sequence
                                                                                                        treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                             The present invention relates to GLUTX proteins (AAF55865-AAF55871 and
                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                   Thorens
                                                                                                                                                                                                                                                                                                                                         (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF55865
                                                                                                                                                                                                                                                        Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF55865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                prevention, diagnosis and . ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laAlaPheCysIleLeuSerValLeuPheThr
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                                                                                                                                                                                                                                                                                           2001-112615/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55865
                                                                                                                                                                                                        3; Page 70-71; 124pp; English.
                       Quality:
                                                                                                                                                                                                                                                                                                                   æ
                                                                                                                                                                                                                                                      acids encoding GLUTX glucose transporter proteins, useful in
                                                                                                                                                                                                                                                                                 AAB66932
                                                                         2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA;
                                                                                               GLUTX1.
                                                                                                                                                                                                                                                                                                                   Ibberson M,
                                                                                                                                                                                                                                                                                                                                                                2000US-0184285
2000US-0616132
                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-IB01042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                        99US-0143907.
99US-0151140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose metabolism disorder; neurodegenerative
454.00
4.882
98.936
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                                                                       750
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                                                                                                                                                                                                                                          treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                       672 G;
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84.043
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                                                                       0 other;
                                                                                                                                                                                                                                        transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                         coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT;AAA44914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antilicer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                         Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag; EST; probe; chemotactic; proliferative;
immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic
thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGGGGGGCCCATCCCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCTTTCTGCATCTTCAGTGTCCTTTTCACT 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGCTTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL
                                                       Page 586; 803pp; English
                                                                                                                                                                                                     McCoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                              98US-0104436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag SEQ ID NO:1489
                                                                                                                                                                                                                                                                                                                               99WO-US24206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA; 579 BP
                                                                                                                                                                                                                         LaVallie ER,
                                                                                                                                                                                                      Bowman MR;
                                                                                                                                                                                                                         Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analgesic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1630
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                                                                                                                                                                                                                       Evans
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sequence tags (sESTs),

to AAA45925 represent specifically claimed secreted expressed tags (sesTs), isolated from human, mouse, chicken and rat

WO200102568-A2

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF67134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-516-493-12 x AAA44914/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression an psoriasis. AAA45926 to AAA45931 represent linker variants which are giv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                            Human; cytostatic;
breast cancer; lunc
                                                                                                                                                                                                                                      AAF67134;
                                                                                                                                                                                                                                                                           AAF67134 standard; cDNA; 378
                                                                                                                                                                                                                                                                                                                                                                              214
                                                                                                                                                                                                                                                                                                                                                                                                                                                          264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 TCTCGCTCCCACAGGCTTTGCGGTGGGGCTGGGGGCCCATCCCCTGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 CCTGCGGACCCTGATGCCTGTCTTGCC......rG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene
                                                       Homo sapiens.
                                                                                                                                                      Novel human polynucleotide, SEQ ID NO:
                                                                                                                                                                                             09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 579 BP; 109 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemotactic; proliferative; immunomodulatory; haematopoietic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMetCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyVal
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                                                                                                                                                                                                                                                                                                                                                                            CAGCCTCATG 205
                                                                                                                                                                                                                                                                                                                                                                                                                   nSerIleMet 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCGACAGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGTCCTCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAG
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                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reverse of: AAA44914
                                                                                            lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266.50
4.675
81.429
                                                                                            gene therapy; colon cancer
g cancer; cancer detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 G; 106 T; 0 other;
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                                                                                                                   cancer;
                                                                                                                                                          2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.
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alignment_block:
US-09-516-493-12 x AAF67134
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                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-1999;
02-JUL-1999;
230
                                                                   181
                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 45 A; 130 C; 117 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                85
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                                                                                                                                                                                                                                                                        31 CTCTTCATCATGGGCTACGCCGTGGGCTGGGGTCCCATCACCTGGCTGCT
                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                      35 uMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyValC
                                                                CCAGTGGT.GAGCACCTTCGGCCTCCAGGTGCCTTTCTTCTTCTTCGCGG
                                                                                                                                                                    ysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAsn
                                                                                                                                                                                                      CATGTCTGAGGTCCTGCCCTGCGTGCCCGTGGCCTCGGCCTCAGGGCTCT
                                                                                                                                                                                                                                                                                            LeuPheIleAlaGlyPheAlaValGlyTrpGlyProJleProTrpLeuLe
CCATCTGCTTGGTGAGCCTGGTGTTCACA
                                                                                                SerIleMetGluileLeuArgProTyrGlyAlaPheTrpLeuThr.AlaA
                                                                                                                                    laPheCysIleLeuSerValLeuPheThr 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Page 974; 1046pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises
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Randazzo F,
R, Drmanac S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US18374
                                                                                                                                                                                                                                                                                                                                              AAF67134
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99US-0142311.
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3.348
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3351 human polynucleotide sequences
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Dickson M,
LW, Strache
                                                                                                                                                                                                                                                                                                                                              from: 1
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Percent Identity: 59.740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nedy GC, Pot D, I
ckson M, Labat I,
Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                              to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions to
                                                                                                    85
                                                                                                                                  180
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA23461

invention may be used in chromosome mapping, and as a source

or

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_documentation_block:
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24-AUG-1998;
09-SEP-1998;
28-SEP-1998;
28-SEP-1998;
25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
                                                                               regime. Diseases or conditions that may be treated using the proteins inucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV: multiple sclerosis; rheumaticid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns,
                                                                                                                                                                                                                                                                                                    The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                              ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may
               additionally be useful as contraceptives. Nucleic acid sequences
                                                                                                                                                                                                                                                      activin/inhibin activity; chemotactic/chemokinetic activity;
                                                                                                                                                                                                                                                                                       cytokine activity; cell proliferation; differentiation; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               blood disorder; haemophilia; autoimmune disease; diabetes; in infection; fungal; bacterial; viral; HIV; allergy; arthritis;
                                                                                                                                                                                                    inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy
                                                                                                                                                                                                                                       and thrombolytic activity; anti-inflammatory activity; and tumour
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 86; Page 335; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative disease; asthma; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human secreted protein vql_1, SEQ ID NO:77.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALPH-) ALPHAGENE INC.
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                                                                                                                                                                                                                                                                      haematopoiesis regulation; tissue growth activity;
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98US-0097659.
98US-0099618.
98US-0102092.
98US-0113645.
98US-0113645.
98US-0379246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US19351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human secreted protein vq1_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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                                                                                                                                                                                                                                                           haemostatic
                 of the
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diagnostic primers and encoding one of the 40

present sequence represents cDNA the invention.

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seq_name:
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                                                                                                                                                                                                                                                             Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
   Nucleic acid molecules
                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                  22-MAR-2000; 2000WO-US07505
                                                                                                                                                                                                                                                                                                                                       Human secreted protein gene 39 SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                                                                                                               AAC80569 standard; cDNA; 1577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laPheCysIleLeuSerValLeuPheThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC80569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                    system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: AAA23461
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .GAGCACCTTCGGCCTCCAGGTGCCTTTCTTCTTCTTCGCGG
                                                                                                                99US-0126502.
99US-0172410.
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3.348
85.714
                                                               Komatsoulis
 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes. The proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 C;
                                                                                                                                                                                                                                                   aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 77
Gaps: 1
Percent Identity: 59.740
                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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  human
                                                                                                                                                                                                                                                    chemotaxis; ss
                                                                G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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secreted proteins,
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  used
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organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacteria, viruses and fungi and ocular disorders e.g. corneal infection The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous \frac{1}{2} \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( \frac{1}{2} \right) \left( 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
Sequence 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disorders e.g. Alzheimer's disease, infections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of their activities include immunosuppressive; antiarthritic;
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352 A;
496
C;
445
G; 284 T; 0 other;
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                                                                          SerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThr.AlaA
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                            laPheCysIleLeuSerValLeuPheThr
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seq_documentation_block:
ID AAF55870 etand...

cDNA; 1541

ВР

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55870

DEXX

17-APR-2001 AAF55870;

(first entry)

Human GLUTX3 coding sequence

seq_name:

/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55871

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alignment_block:
US-09-516-493-12 x AAF55870
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23-FEB-2000;
13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUTI-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 81-82; 124pp; English.
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CCATCTGCCTGGTGAGCCTGGTGTTCACA
                                     laPheCysIleLeuSerValLeuPheThr
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                                                                                                           SerIleMetGluIleLeuArgProTyrGlyAlaPheTrpLeuThr.AlaA 85
                                                                                                                                                                     ysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPheAsn 68
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2000US-0616132.
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alignment_block: US-09-516-493-12 \times AAF55871
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                                                                                  1153 CCAGCCGCGCCTTCAACTATCTCACCCTGATACCCCTGCTGCCGCCACCAT
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                          function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 82-83; 124pp; English.
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euMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyVal
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seq_documentation_block:
ID AAC40459 standard; DNA; 1755 BP
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                                                                                                                                                                                                                                             cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; esteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                       neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                    antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                        26-JUL-2001
                                                                                                                                                                                                                               Alzheimer's disease; Parkinson's disease; neurodegenerative disorder:
                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein encoding cDNA sequence SEQ ID NO:498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
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                                                                                         22-DEC-2000;
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Ratio:
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                            99US-0471275.
2000US-0488725.
2000US-0552317.
                                                                                        2000WO-US35017
                                                                                                                                                                                                                  disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               HIV infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ion; human immunodeficiency virus;
antiarthritic; immunosuppressive;
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immunosuppressive;

infection;

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alignment_scores

(HYSE-) HYSEQ INC

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seq_documentation_block:
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AC AAC45857;
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DE Arabidopsis thaliana
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US-09-516-493-12 x AAH99663
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiulcer osteopathic; dermatological; antialtergic; antiactmatic; antiparkinsonian; and immunostimulant. The proteins and polynucleotices encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arrhritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fingicide; antimutagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH99166 to AAH99504 CAAM25963. The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 564; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 421 BP; 72 A; 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorders.
                                                                                                                                                                      151
                Arabidopsis thaliana DNA fragment SEQ ID NO: 48015
                                                                                                  AAC45857 standard; DNA; 1395 BP
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                                                                                                                                                                                                                               GTGGCGTGGCCTCAGGGCTCTGCGTGCTGGCCAGCTGGCTCACCGCCTTC
                                                                                                                                                                                                                                               ysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPhe
                                                                                                                                                                      GTCCTCACCAAGTCCTTC 168
                                                                                                                                                                                                                                                                                                                                            CTCGCAGGCCGCAAGGTGCTGCTCTTCGTCTCAGGCTACGTCGTGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH99904 encode the human proteins given in AAM25225 to he proteins can have activities based on the tissues and
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189.00
3.780
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AACTCGTTGGCCCGGAGGCTGTCGGCGCCCCACAGAGCTGGGCCCCTGGGA 1855
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alignment_block:
US-09-516-493-12 x US-08-928-692-9
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-368-431-15
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-368-431-17
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-71
                                                                                                                                                                         Align seg 1/1 to: US-08-928-692-9
                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                        1706 ATCTACTTCAACCTGAAAGCCTTATCCGCCATAGCAGTTCTACTTTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lamsa, Micha
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                          21 eAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerG
                                                                                                                                       5 ValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIl
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DLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                       linear
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1856 GCGAACTGGATTGCCACGTTCATCGTGGCACAATTTTTTCCGATGTTAAA 1905

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; OTHER INFORMATION: modified GLUT4 containing myc tag sequences US-09-591-025-8
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SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/138,237 PRIOR FILING DATE: 1999-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/591,025
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/154,078
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Method of Measuring Plasma Membrane
TITLE OF INVENTION: Targeting of GLUT4
FILE REFERENCE: 0399.1210-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                             1503 GATTGGCCCTGGCCCCATTCCTTGGTTCATCGTGGCCGAGCTCTTCAGCC 1552
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                                                1653 GCCCTAC...GTCTTCCTTCTATTTGCGGTCCTCCTGCTGGGCTTCTTCA 1699
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92 euPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAl 25
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                                                                                            gProTyrGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValL 92
                                                                                                                                                                                           MetAlaPheLeuValThrLysGluPheAsnSerIleMetGluIleLeuAr 75
                                                                                                                                                                                                                                                                                    euHisIleLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPhe 58
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Ratio:
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alignment_block:
US-09-516-493-12 x US-08-998-416-719/rev
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                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                         ; ORIGINAL SOURCE:
; ORGANISM: PAG
US-08-998-416-719
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                                                                                                                                         Align seg 1/1 to reverse of: US-08-998-416-719
                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 TCTTCACC 1707
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                   536 TGCCTCTACATTTTTCTTCTTTGCAACTACCTGGGCCCCCAATTGCGTATG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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486 TCATTGTTTCGGAGACTTTCCCATTAAGAGTCAAAGCCAAGGGCATGGCT 437
                               34 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly 50
                                                                                                     18 CysLeuPheIle.AlaGlyPheAlaValGlyTrpGlyProIleProTrpL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 24-DE
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ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                     Quality:
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1: 3054 Cornwallis Road
Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708 base pairs
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Steiner, Sabine
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Knechtle, Philipp
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29.870
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ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh

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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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; Sequence 1, Application US/09103840A
; Patent No. 6294328
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-031-392-1
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                                                            3718455CGTTCGCCGTCGTCGCG 3718471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 uPhelleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuM 36
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                                                                                                                        laPheCysIleLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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67.416
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alignment_block:
US-09-516-493-12 x US-09-031-392-1
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; LOCATION:
US-09-031-392-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                         1459 TTTGCTGTTGGGCTCCTCTTCCCATTCATTCAGAAAAGTCTGGACACCTA 1508
                                                                                                                                                                                                                                                                                    1309 TACCTGAGTATCGTGGGCATTCTGGCCATCATCGCCTCTTTCTGCAGTGG
                                                                                                                       1409 AGCGGCCGGCTGCCTTCATCATTGCAGGCACCGTCAACTGGCTCTCCAAC 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09 FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tartaglia, Louis A. APPLICANT: Weng, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                           61 PheLeuValThrLysGluPheAsnSerIleMetGluIleLeuArgProTy 77
                                                                                                                                                                                                                                          27 yTrpGlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHis1 44
                                                                                                                                                                                                                                                                                                                         11 TrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGl 27
77 rGlyAlaPheTrpLeuThrAlaAlaPheCysIleLeuSerValLeuPhe 93
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TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meiklejohn, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                      GCCAGGTGGCATCCCGTTCATCTTGACTGGTGAGTTCTTCCAGCAATCTC 1408
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Percent Identity:
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seq_documentation_block:

Sequence 1 Patent No.

, Application US/09299549 6136547

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A. APPLICANT: Weng, Xun

seq_name:

1509

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alignment_block: US-09-516-493-12 \times US-09-299-549-1
                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-09-299-549-1
                                                                                                                                                                                Align seg 1/1 to: US-09-299-549-1 from: 1
                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                               1359 GCCAGGTGGCATCCCGTTCATCTTGACTGGTGAGTTCTTCCAGCAATCTC 1408
                                                                                                               1309 TACCTGAGTATCGTGGGCATTCTGGCCATCATCGCCTCTTTCTGCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/031,392 FILING DATE: 26-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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44 leLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAla 60 ::: :::|||||
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TELEFAX: DI.,
TELEFAX: SE/
                                                                                                                                               11 TrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGl
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alignment_block:
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                                                                                                       Align seg 1/1 to: US-08-948-564-9
                                                                                                                                           US-09-516-493-12 x US-08-948-564-9
                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1459
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                                   141 GGAGGAGCATGGCCAATTATTGGCCATTTACACCTCTTTGGGGGGTCATCA 190
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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GlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPhe.....
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                                                                                                                                                                                                                                  Quality:
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No. 6121512th Carolina
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Corbin, Frederick T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Siminszky,
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Percent Identity: 25.773
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Gaps:
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seq_documentation_block:
;Patent No. 5449756
; Patent No. 5449756
; APPLICANT: TANIGUCHI, TADATSUGU;HATAKEYAMA, MASANORI;MINAMOTO,
;SEJIRO;KONO, TAKESHI;DOT, TAKESHI;MIYASAKA, MASAYUKI;TSUDO,
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;Patent No. 5198359
                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5449756-3
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;MITSURU;KARASUYAMA, HAJIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-MAR-1990
:SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TANIGUCHI, TADATSUGU;JATAKEYAMA, MASANORI;
MINAMOTO, SEJIRO:KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;
TSUDO, MITSURU;KARASUYMA, HAJIME
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APPLICANT:
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CURRENT APPLICATION DATA:
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                                                                                                                                                             TACCTGCCTCCTT 2262
                                                                                                                                                                                                 yValCysValLeu 54
                                                                                                                                                                                                                                           TTAGTCATG
                                                                                                                                                                                                                                                                               LeuLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGl 50
                                                                                                                                                                                                                                                                                                                       TTGGTGGAGGGTGGGAGTGGGGAGCGGTGGTCAGCTCCACTGCCCTAT 2223
                                                                                                                                                                                                                                                                                                                                                           TAATCATCCACTTCTGAACTCCATTTGCTACTTCCTGGTCTAACCAGGGT 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                         .................ValGlySerMetCysLeuPheIleAla......GlyP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTATGCCATGTTTGGCTTCACTCCTTATGGTCCTTATTGG 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ProTrpLeu 34
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Gaps: 5
Percent Identity: 29.577
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 209, Application US/08781891 Patent No. 6090620
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APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,891
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 865,155
FILING DATE: 08-APR-1992
APPLICATION NUMBER: 487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2 NUMBER OF SEQUENCES: 12 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                CITY: Seattle
STATE: Washing
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                                                                                                                                                         COUNTRY:
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                                                                                                                                         98104-7092
                                                                                                                                                                          Washington
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                                                                                                                                                                                                                    6300 Columbia Center,
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1.961
53.521
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US/08/781,891
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Percent Identity: 29.577
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                                       Version
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alignment_block:
US-09-516-493-12 x US-08-781-891-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-176-620A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 5595904
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 rAsnTrpPheMetAlaPheLeuValThrLysGluPheAsnSerIleMet 71
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION:
                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
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STRANDEDNESS: single
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1.674
64.179
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seq_documentation_block:
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US-09-516-493-12 x US-08-176-620A-1/rev
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US-08-176-620A-1
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                                                                                                                                                                                                                                                                          Sequence 1, Application US/08463862 Patent No. 5776751
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027 TGGGGAGATCATCCAGCTCCATGTCAAA.....
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                       COMPUTER READABLE FORM:
                                                                                                                                                                                                             APPLICANT: Boulton, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                     989 TCCTCAGCCACTGGTTCATCTGTCGGATCATA 958
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                                                                                                                                                                                            NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
                                                                                      STATE:
                                                                                                                                              ADDRESSEE:
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TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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                                                                                    New York
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1.905
39.362
                                                                                                                                                                                                               A FAMILY OF MAP2 PROTEIN KINASES
                                                                                                                                                                                                                                   Teri G. et al
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Percent Identity: 25.532
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36 tSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyValCysV 53 ::::      :::      :::
33 TrpLeuLeuMe 36
16 erMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIlePro 32 ::          :::         1115 AGGGGTGTCTGTTGTTAGGGGGGCCTCTGGTGCCCC 1078
14valglys 16
7 LeuGlyLeuAlaTrpLeuAla
Align seg $1/1$ to reverse of: US-08-461-985-1 from: 1 to: 174
alignment_block: US-09-516-493-12 x US-08-461-985-1/rev
alignment_scores: Quality: 70.50 Length: 94 Ratio: 1.905 Gaps: 5 Percent Similarity: 39.362 Percent Identity: 25.532
URE: ME/KBY: CDS CATION: 11095
nucleic acid EDNESS: sing GY: unknown TYPE: DNA (
MATION FOR SEQ ID UENCE CHARACTERIST ENGTH: 1747 base
TELEPHONE: (212) 790-9090 TELEFAX: (212) 869-8864/97 TELEX: 66141 PENNIE
REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 6526-123 TELECOMMUNICATION INFORMATION:
O3-JAN-1994  'INFORMATION:
A: 0
CURRENT APPLICATION DATA:  APPLICATION NUMBER: US-/08/461,985  FILING DATE: 05-JUN-1995
OPERATING SYSTEM: PC-DOS/M SOFTWARE: PatentIn Release
PE: Floppy disk IBM PC compatible
IP: 10036 PUTER READABLE FORM:
TATE:
ESSEE: Pe
R OF SEQUENCES: 21 SPONDENCE ADDRESS:
APPLICANT: NYE, SLEVEN APPLICANT: Panayotatos, Nikos TITLE OF INVENTION: A Family of Map2 Protein Kinases
LICANT:

989 TCCTCAGCCACTGGTTCATCTGTCGGATCATA 958

53 alLeuThrAsnTrpPheMetAlaPheLeuVal 63

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33 TrpLeuLeuMe 36	16 erMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIlePro 32 ::	14ValGlyS 16	7 LeuGlyLeuAlaTrpLeuAla	Align seg $1/1$ to reverse of: US-08-932-787B-1 from: 1 to: 1747	alignment_block: US-09-516-493-12 x US-08-932-787B-1/rev	alignment_scores:  Quality: 70.50  Ratio: 1.905  Percent Similarity: 39.362  Percent Identity: 25.532	NAME/KEY: CDS  LOCATION: (1)(1095)  OTHER INFORMATION: ERK1 cDNA  US-08-932-787B-1	; LENGTH: 1147 ; TYPE: DNA ; ORGANISM: RAT	NUMBER OF SEQ ID NO. SOFTWARE: FastSEQ SEO ID NO 1	PRIOR FILING DATE: 1991-05-16 PRIOR APPLICATION NUMBER: 07/532, PRIOR FILING DATE: 1990-06-01	PRIOR PRIOR	CURRENT FILING DATE: 1997-09-18 PRIOR APPLICATION NUMBER: 08/469,547 PRIOR FILING DATE: 1995-06-06	TILE OF INVENTION: KINASES FILE REFERENCE: REG 430-A-1 CURRENT APPLICATION NUMBER: US/08/932,787B	eq_documentation_block eqquence 1, Applicati Sequence 1, 27963 Patent No. 6277963 GENERAL INFORMATION: APPLICANT: Boulton TITLE OF INVENTION:	<pre>seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-932-787B-1</pre>	53 alLeuThrAsnTrpPheMetAlaPheLeuVal 63 ::   :::::      :::::::::::::::::::::	36 tSerGluIlePheProLeuHisIleLysGlyValAlaThrGlyValCysV 53 ::::      :::	33 TrpLeuLeuMe 36                1077 TGGCTGGAAGCGGGCTGTCTTGGAAGATCAGCTCCTTCAGCCGCTCCT 1028	16 erMetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIlePro 32 ::        :::     1115 AGGGGTGTCTGTTAGGGGGGCCTCTGGTGCCCC 1078

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Database: EST:*
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-Q-/Cgn2_1/USOPTO_spool/USO9516493/runat_13022002_125122_18425/app_query.fasta_1.894
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| BF120840 601757442F1 NCI_CGAP_M
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| BG290178 602385265F1 NIH_MCC_93
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| BF744206 283798 MARC 3B0V Bos to AL565390 LTI_FL013_FB1
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AW940827 GH21190 3prime GH Dros
B6586896 EST488665 MHAM Medicaq
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A1999333 701555458 A. thaliana,
BED20975 sm54b09.y1 Gm-c1028 GI
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BF033803 601454148F1 NIH_MGC_66
C88387 C88387 Carp alginate-inc
BI422148 EST532814 tomato callu
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BG591090 EST498932 P. infestans
BE458971 EST414263 tomato devel
BE021773 sm62c10 y1 Gm-c1028 G1
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BG749509 602707648F1 NIH_MGC
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9712, Medical Center
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                            (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse
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EST111406 Rat PC-12
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For clone availability please contact
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,A.R., Fraser,C.M. and Venter,J.C.
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/organism="Rattus sp."
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/db_xref="taxon:10118"
/db_xref="taxon:10118"
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/clone_lib="Rat PC-12 cells, NGF-treated (PC-12 cells, NGF-treated PC-12 cells, NGF-treated PC-12 cells. CDNA was purified from 9-day NGF treated PC-12 cells. CDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"

80 g 88 t 1 others
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Sic Kit
Technologies).
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503.00 5.409 98.936 Percent Identity: 98.936 Length: Gaps:

Align seg 1/1 to: H34451 from: 1 to: 319

1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe 68

tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL GTGCCTCTTCATCGCTGGTTTTGCAGTAGGCTGGGGACCCATCCCCTGGC 50

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alignment_block:
US-09-516-493-12 x BE231636
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                      1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe
ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Tex: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                       Quality:
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for
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                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20 and 30 embryos."
182 c 162 g 124 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="MARC 1PIG"
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                                                                                                                                                                                           458.00
4.925
98.936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/db_xref="taxon:9823"
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LOCUS BG749509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
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                                           Quality:
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High quality sequence stop: 745.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 949)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602707648F1 NIH_MGC_43 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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BG749509.1 GI:14060162
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                      Ratio:
                                                                                                                                                         160
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                                                                                                                                                                       note "Organ: eye; Vector: pOTB7; Site_1: xhoI, EcoRI; cDNA made by oligo-dr priming. Direct cloned into EcoRIXhoI sites using the folloadaptor: GGCACGAG(G). Library constructed in the laboratory of Gerald M. Rubin (Univer California, Berkeley) using ZAP-CDNA synth (Stratagene) and Superscript II RT (Liff (Note: this is a NH_MGC Library. | "
4.914
98 936
                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4844411"
/clone_lib="NIH_MGC_43"
/tlssue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9192 row: d column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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/note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: Sall Site_2: Not1; Cloned unidirectionally. Primer: Oligo do Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3986651"
                                                                                             /clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                              Primer: Oligo dT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BE910478
BE910478.1 GI:10407108
                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The Inm. A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://limage.llnl.gov
Plate: LLAM9706 row: i column: 01
                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 934)
                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3903048"
/clone_lib="NIH_MGC_70"
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LOCUS BG290178
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                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10402 row: a column: 17
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                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                    Unpublished (1999)
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                quality sequence stop:
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/lab_host="0H10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGTCCTTTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpPheMetAlaPheLeuValThrLysGluPheAsnSerIle.MetGluI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCTATGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est1:AL565390
                                                                                                                                                                                                                                                                                                                                                         AL565390 T1_FL013_FBrn1 Homo sapiens cDNA clone CSODF005YE02
                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                  Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                          AL565390
                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                     AL565390.1 GI:12916718
                                                                                                                                                                                                                                                                                                                                           prime, mRNA sequence
                                                                                                                                                                                                                                                                  numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                               (bases 1 to 752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG290178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/dlone="IMAGE:4514200"
/clone="IMAGE:4514200"
/clone=lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pcMV-SPORT6; Site_1: Notl
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401.00
4.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                            Jessee, J. and Polayes, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 g
                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 712
                                                                                                                                           normalization
                                       Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
1
86.517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
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DEFINITION ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BF774206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:BF774206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AL565390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-516-493-12 x AL565390/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sGluPheAsnSerIleMetGluIleLeuArgProTyrGlyAlaPheTrpL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tCysLeuPhelleAla...GlyPheAlaValGlyTrpGlyProIle.Pro 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCCTCCGCTTTCTGCATCTTCAGTGTCCTTTTCACT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euThrAlaAlaPheCysIleLeuSerValLeuPheThr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGTTCAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGGCATCTGCGTCCNCACCAACTGGCTCATGGCCTTTCTCGTGACCAA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrGlyValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCTCTTTCNATCGCCNGCTTTTGCGGTGGGGCTGGGGGCCCATCCCCT 616
                            1 (bases 1 to 440)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., G.L., 
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF774206.1 GI:12122106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF774206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283798 MARC 3BOV
                                                                                                                                                                                                                                    Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ø
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4.197
90.816
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fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
http://fulllength.invitrogen.com"
a 206 c 242 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: Fetal brain: Vector: pCMVSPORT 6: 1st strancDNA was primed with a NotI-ollgo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="pooled tissue from post conception letuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODF005YE02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="LTI_FL013_FBrn1"
Holt,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus cDNA 5', mRNA
                                                                                                                                                                                                                                    Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 98
Gaps: 4
Percent Identity: 75.510
Karamycheva,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
Liang, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     others
Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1st strand
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665

17

 $\omega$ 

VERSION KEYWORDS

465

515

82

565

65

49

SOURCE

REFERENCE

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COMMENT
                                                                       DEFINITION
                                                                                                                                                 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
 KEYWORDS
                     VERSION
                                    ACCESSION
                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-516-493-12 x BF774206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                               379
                                                                                                                                                                                        429
                                                                                                                                                                                                                                                                                                                                       329
                                                                                                                                                                                                                                                                                                                                                                                                                   279 GTGCCTCTTCATCGCCGGCTTCGCTGTGGGGTTGGGGGCCCCATCCCGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                 51 ValCysValLeuThrAsnTrpPheMetAlaPheLeuValThrLysGluPh
                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                            34 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                  17 tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe
                                                                                                                                                                                                                           eAsnSerIle
                                                                                                                                                                                        CAGCAGTCTC 438
                                                                                                                                                                                                                                                               GTCTGCGTCCTCACCAACTGGTTCATGGCCTTTCTGGTGACCAAAGAGTT
                                                                                                                                                                                                                                                                                                                                       TCCTCATGTCTGAGATCTTCCCTCTGCATGTCAAGGGCGTGGCCACCGGC
                                                                                                                                                 gb_est1:AW248655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscoruland -minmatch 12 options.
                                  mRNA sequence.
AW248655
                                                                         AW248655 496 bp r
2820759.3prime NIH_MGC_7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PO Box 166,
Tel: 402 76
AW248655.1 GI:6591648
EST.
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Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
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a 141 c 135 g 99 t
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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/lab_host="DH10B"
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5.087
98.571
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Gaps:
Percent Identity:
                                                                                             mRNA
                                                                         Homo sapiens cDNA clone IMAGE: 2820759
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BASE COUNT
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US-09-516-493-12 x AW248655/rev
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TITLE
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305 ATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTT
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                                                 51
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                        euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly
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Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
scores: PHRED from University of Washingtion Genome Center: Vector
Trimming: cross_match from University of Washingtion Genome Center:
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
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Other_ESTs: 2820759.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 496)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: Recorl; cDNA made by oligo-dT priming. Directionally EconI; cGNA made by oligo-dT priming. Directionally cloned into EconI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 145 c 142 g 92 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2820759"
/clone_lib="NIH_MGC_7"
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4.875
97.297
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/cell_line="MGC3"
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Gaps: 0
Percent Identity: 83.784
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to:
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MEDLINE
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AUTHORS
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US-09-516-493-12 x BF742266/rev
                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
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                                                                                                                                                                     Percent Similarity:
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                                                           Align seg 1/1 to reverse of: BF742266
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 327)

Veriovski-Almeida, S., Briones, M.R
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RC1-BTN0409-021000-012-e12 BTN0409 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BTN0409
-021000-012-e12&t3=2000-10-02&t4=1)
Seq.primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
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                                                                                                                                                                                                             Quality:
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                                                                                                                                                                                                                                                                                                                                                           /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                     stringency conditions."
91 c 108 q
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4.527
91.250
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/db_xref="taxon:9606"
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Percent Identity:
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alignment_block:
US-09-516-493-12 x BF140667
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Align seg 1/1
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                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia;
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EST.
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601786917F1 NCI_CGAP_Lu30 Mus musculus
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Plate: LLAM9259 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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to:
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BF140667
                                                                                                                                                                                                                 /note="organ: lung; Vector: pCMV-SPORT6: Site_1: NotI: Site_2: Sall; transgenic model wNT-1, expression driven wMTV-LTR enhancer; Cloned unidirectionally. Primer: O.dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" a 263 c 277 g 214 t
                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
                                                                                        299.00
4.333
97.183
                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4014605"
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from: 1
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Sciurognathi; Muridae;
917
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Murinae; Mus
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65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF146289 235 bp mRNA EST 26-OCT-2000
EST000181 rabbit blastocyst mRNA to cDNA Oryctolagus cuniculus cDNA
clone G81 similar to glucose transporter 8 (GLUT8), mRNA sequence.
BF146289
BF146289.1 GI:11027684
                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Anatomy and Cell Biology
Martin Luther University Halle-Wittenberg,
Grosse Steinstrasse 52, D-06097 Halle, GER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kietz,S., Augustin,R. and Fischer,B.
Expression of glucose transporters in rabbit preimplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rabbit.
Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: silke.kietz@gmx.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          embryos
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(bases 1 to 235)
                                                                     to:
                                                                                                                                                                                                                                                                          39
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                                                                                                                                                                                                                                                                        /dev_stage="six days old preimplantation embryo"
78 c 61 g 57 t
                                                                                                                                                                                                                                                                                                        /clone="G81"
/clone_lib="rabbit blastocyst mRNA to cDNA"
                                                                                                                                                    285.00
4.750
98.361
                                                                                                                                                                                                                                                                                                                                          /strain="hybrid strain Zika"
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryctolagus
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1 (bases 1 to 295)

1 (bases 1 to 295)

1 (bases 1, Califton, S., Johnson, S., Li, F., Marra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R. Washl Zebraish EST Project 1999
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BG303512.1 GI:13101039
EST
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG303512 295 bp mRNA EST 23-FEB-2001 f156g08.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 3817934 3' similar to TR:Q9V610 Q9V610 CG8234 PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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                       87
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314 286 1810
             [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGT). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage resistant)"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
                                                                                                                                                                                                                                                                                                                                                                                                      /sex="mixed (one male and one female, unfertilized eggs)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7955"
/clone="3817934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano Kawakami zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           including
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63108,
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                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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alignment_block:
US-09-516-493-12 x BG303512/rev
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LOCUS BG079217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BG079217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 TATTGGTTGGGGTCCTACTCCGTGGCTGATGTCAGAGATCTTCCCCA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TGTGCCTTCATTGACACCAAAACCTTCCAGAACCTCATGGATGCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 CTGGCCTGGTTGTCTGTGGATAGCATGGGCTTTTTCATTGCAGGATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 CGCGGGTGAGGGGATTAGGCAGTGCTCTGTGTGTGCTTACTAACTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 euPheThr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 CAGCGCAGGAACATTTTGGATGTTCTCGGCACTGTGTGCTTCTAATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 MetAlaPheLeuValThrLysGluPheAsnSerIleMetGluIleLeuAr 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 euHisIleLysGlyValAlaThrGlyValCysValLeuThrAsnTrpPhe 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAl
                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
plate: H3037 row: C column: 03
Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H3037C03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3037C03 5', mRNA sequence.
BG079217
                                                                                                                                                                                                                                                                                                                                               Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Other_ESTs: H3037CO3-3
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                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verification and initial annotation of NIA mouse 15K cDNA clone set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K.,
,T.S., Carter,M.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
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                                                                                                                                                                                                     quality sequence stop:
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="H3037C03"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
                                                                                                                                                       Location/Qualifiers
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3.972
82.558
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Gaps: 0
Percent Identity: 55.814
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                                                                                                                                                                                                                                                                                                                                                          USA
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Please

/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA

/lab_host="DH10B" libraries"

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REFERENCE
AUTHORS
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KEYWORDS
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US-09-516-493-12 x BG079217
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Ratio: 5.192
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 GTGCCTCTTCATTGCTGGCTTTGCGGTGGGGTGGGGACCCATCCCCTGGC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 euLeuMetSerGluIlePheProLeuHisIleLysGlyValAlaThrGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 tCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ValCys 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GluProAlaAspValHisLeuGlyLeuAlaTrpLeuAlaValGlySerMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTCATGTCAGAGATCTTCCCTCTGCATGTCAAGGGTGTGGCTACCGGC 58:
Distinct gene expression profiles of rat dorsal root ganglion induced by peripheral nerve axotomy
                                                                                                                           1 (bases 1 to 538)
Xiao,H.S., Han,Z.G., Zhang,F.X., Huang,Q.H., Lu,Y.J., B., Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G.,
                                                                                                                                                                                                                                                                                                                                                                                               Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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BG672321.1 GI:13894420
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                                                                                           Zhang, X.
                                                                                                                                                                                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG672321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are cloned unidirectionally with Oligo(dT source libraries are clon
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177 c 182 g 141 t
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clone is among a rearrayed set of 15,247 clones from 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 bp
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0
90.385
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                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                 Murinae;
                                                                                                                               Bao, L., Fi
                                                                                                                                                                             Fu,G.
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SOURCE

TITLE

ORIGIN

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alignment_block:
US-09-516-493-12 x BG672321
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                62 euValThrLysGluPheAsnSerIleMetGluIleLeuArgProTyrGly 78
                                                                                                                                                                               45 sGlyValAlaThrGlyValCysValLeuThrAsnTrpPheMetAlaPheL
                                                                                                                                                                                                                                                             29 GlyProIleProTrpLeuLeuMetSerGluIlePheProLeuHisIleLy
                                                                                                                                                          55 GGGGGGGGTACCGGGGTCTGGGTCCTCACCAACTGGTTCATGGGCTTTC 104
                                                                                                                                                                                                                                         5 GGACCCATTCCCTGGCTTCTTATTTCAAAGAACTTTCCTTTGCACAATAA 54
                                                                              TGGGGACCAAAGAGTTTAACAGCATCATGGAGAATCTTAAACCCTACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 Yue Yang Road, Shanghai 200031, P.R.China Tel: 86-21-64748700-121
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The Institute for Geno
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9712, Medical Center D
Fel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability
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EST111406 Rat PC-12 cells, NGF-treat
end similar to Glucose transporter,
H34451
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Comparative expressed sequence tag analysis of differential expression profiles in PC-12 cells before and after nerve given the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the seq
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nhlee@tigr.org
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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e, Rockville,
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before and after nerve growth
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798 HWM0002.F0
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             University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
                                                                                                                  Genome Res. 6 (9), 791-806 97044477
                                                                                                                                                                                                                                                                                                                    BF551290 426 bp mRNA EST 12-DEC-2000 UI-R-CO-hq-f-01-0-UI.rl UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-hq-f-01-0-UI 5', mRNA sequence.
                                                                                     Contact: Soares, MB Program for Rat Gene
                                                                                                                                                                           Bonaldo, M.F.,
                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
 cDNA Library Preparation:
                                                                                                                                                discovery
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/db_xref="taxon:10118"
/db_xref="taxon:10118"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript SK-: Site_1: EcoRI; Site_2: XhoI; poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"
a 102 c 80 g 88 t 1 others
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99.4%;
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Pred.
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Soares Lab Clone distribution:
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   REFERENCE
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                                                                                                                                                                                                                              UI-R-BJ2-bpm-c-04-0-UI.sl UI-R-BJ2 Rattus norvegicus UI-R-BJ2-bpm-c-04-0-UI 3', mRNA sequence.
BF420038
BF420038.1 GI:11408077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161;
       Norway rat.
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.lln.agov). IMAGE ID- 1773689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
(bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996)"
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/clone="UI-R-C0-hq-f-01-0-UI"
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/strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 161; DB 11; Pred. No. 1.3e-27;
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KEYWORDS
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AA997295/c
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                                                                                                                                                                                                                                                                                                                                                                                                        245
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                                                                                                                                                                                                                                                                                                                                                                                                        TCAGAAACAAGGTCAGGTGAGTCCAGGAAGAAAAGAGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161;
                                                                                                             AA997295 481 bp mRNA EST UI-R-CO-hq-f-O1-O-UI.S1 UI-R-CO Rattus norvegicus UI-R-CO-hq-f-O1-O-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 Eckstein Medical Research Building Iowa City, IA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                AA997295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence contained an oligo-dT track that was present in oligonucleotide that was used to prime the synthesis of first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                     AA997295.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
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/clone_lib="UI-R-BJ2"
/clone_lib="UI-R-BJ2"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
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/note:-pT73D-Pac (
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105 c 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-R-BJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    visit our web site at ratest.eng.uiowa.edu. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5%; Score 161; DB 11; 0.0%; Pred. No. 1.2e-27;
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MEDLINE
                                                                                                                       Best Local Similarity
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                          634 tgcgggctcctggctctagtgctctggctgtggcatctttgggtgctttggtcctaagcaa 693
           364
  TGCGGGCTCCTGGCTCTAGTGCTCTGGCCTGGCCATCTTTGGGGTGCTTGGTCCTAAGCAA 305
                                                                                                  161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jun 5, 1998 this Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction: two approaches to facilitate gene
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                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                               and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electrony converted to
                                                                                                                                                                                                                                                                                                   bacteria (Life Technologies) to g
library. This procedure has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (Life Technologies)"
/note="Vector: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library_is_a subtracted_library_derived from the UI-R-A1
                                                                                                                                                                                                                                                           1996)"
                                                                                                                                                                                                                                                                                                                                                      double-stranded circles and electroporated into DH10B
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/clone="UI-R-C0-hq-f-01-0-UI"
/clone_lib="UI-R-C0"
                                                                                                                                                                                                                                                                              (Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence version replaced gi:3188156
                                                                                               0;
                                                                                        Score 161; DB 10;
Pred. No. 1.1e-27;
Pred. No. 1.1e-27;
                                                                                                                                                                                                                                     128
                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                been previously described Genome Research 6: 791-8
                                                                                                                                                                                                                                                                                                                         to generate the UI-R-CO
                                                                                                                                      Length 481;
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BI275901/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
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                                                                                          ω
                                                                                 TAG_TISSUE=rat placenta pool
TAG_SEQ=TCACGACAGT"
141 c 163 g 124 t
                                                                                                                                                           TAG_LIB=UI-R-CXO
                                                                                                                                                                                 described in (Bonaldo, 6:791-806, 1996)
                                                                                                                                                                                                                            ratest.eng.uiowa.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="UI-R-CX0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="ADULT"
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15.5%;
Score 161;
DB 11;
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754 tcagaaacaaggtcaggtgagtccaggaagaaaagagaatg 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 Eckstein Medical Research Building Iowa City, IA 52242,
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                                                                                                          /lab_host="DH10B (Life Technologies)"
/note="Vector: pf773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CX0 library is a normalized library constructed from the following rat placenta tissues: embryonic day 17, embryonic day 19, embryonic day 21. For a detailed description of the library from which this clone was
                                                                             derived, please visit our web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-R-CX0-bxh-h-03-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lennon, G. and Soares, M.B.
                                    The subtraction has been previously
Lennon and Soares, Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   facilitate gene
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    Research
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Length 563;

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310 TGCGGGCTCCTGGCTCTAGTGCTCTGGCTGGGCATCTTTGGGGTGCTTGGTCCTAAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tcagaaacaaggtcaggtgagtccaggaagaaaagagaatg 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcgggctcctggctctagtgctctggctgggcatctttggggtgcttggtcctaagcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGAAACAAGGTCAGGTGAGTCCAGGAAGAAAAGAGAATG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti Site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 16.5 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21, Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
451 Eckstein Medical Research Building
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I (bases 1 to 295)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF420257
BF420257.1 GI:11408246
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF420257 295 bp mRNA EST 28-NOV-2000 UI-R-BJ2-bpk-g-03-0-UI.sl UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bpk-g-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat
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                                       /Strain="Sprague-Dawley"
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                          Lennon and Soares, Genome
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                             Research 6:791-806,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 ctcacttgactgggggatgagaaaagggacttagccacataagatttgggctcagaaacaa 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtcaggtgagtccaggaagaaaagagaatg 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., ,R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Ker, A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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H34372.1 GI:979789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone RPNBT28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST111272 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (tdbinfo@tdb.tigr.org)
Seq primer: M13 - 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nhlee@tigr.org
For clone availability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712, Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95396786
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
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                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301)-838-3529
(301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                       Conservative
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                                                                                                                                                                                                                                                     Kit by Stratagene"
1 74 c 79 g
                                                                                                                                                                                                                                                                                                       and directionally cloned using the Lambda ZAP II Vector
                                                                                                                                                                                                                                                                                                                               /clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript Sr.; Site_1: EcoRI; Site_2:
XhOI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="ATCC (inhost):2005377"
/db_xref="taxon:10118"
/clone="RPNBT28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_TISSUE=ventricle at 16.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus sp."
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                                                                                                                             6.8%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score 9; Pred.
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Sciurognathi; Muridae; Murinae;
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. 4.8e-07;
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hes 0;
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REFERENCE AUTHORS TITLE

Rattus.

SOURCE

ORGANISM

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COMMENT

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Genome R 97044477

Contact:

FEATURES

source

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||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801929
Fax: 86-21-50801929
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 723)
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Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
                                                              Homo sapiens
                                                                                             EST
                                                                                                                           AV706527 ADB Homo sapiens cDNA clone ADBCMF12 5', mRNA sequence. AV706527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AV726694 HTC Homo sapiens
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AV726694.1 GI:10836115
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                                                                                                                                                         AV706527
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Song, H.,
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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   Huang, Q.,
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 Huang, C.,
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   Gu,Y.,
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   Yang, Y., Gao, G.,
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                        855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                            Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                University
                                                                                                                                                                                                                                                                                                 Walbot, V
                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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Contact: Zeguang H
                                                                                                                                                                                            Stanford University
                                                                                                                                                                                                                                                                              Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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                                                                                                          Plate:
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351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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                                                                                                                        walbot@stanford.edu
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/organism="Zea mays"
/cultivar="B73" 4577"
/db_xref="taxon:4577"
/clone_lib="496 - stressed shoot cDNA library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBCMF12"
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; Pred. No. 5.1e-06;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 62; Conservative
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AW333608
AW333608.1
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                                                                                                                                                                                                                                                                                                                                                                                            101 Morgan Building, University of Kentucky, 40506-0225, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smulian,A.G., Arnold,J., Weise,M., Wunderl,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pneumocystis carinii f. sp. carinii.
Pneumocystis carinii f. sp. carinii.
Eukaryota, Fungi, Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
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                                                                                                                                                                                                                                                                                                                                                Email: staben@pop.uky.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                        University of Kentucky
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                                                                                                                                                              /note="Vector: Lambda ZAP II: Site_1: EcoR1: Site_2: XhoI: P. Carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/project/Pneumocystis/" a 14 g 90 t
                                                                                                                                                                                                                                                                            /organism="Pneumocystis carinii f./db_xref="taxon:38081" (clone_lib="ACS-1"
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/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
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lab Zea mays cDNA, mRNA sequence.
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100 Jordan Hall, Clemson,
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Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="tomato callus, '
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC6G13"
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                                                                                                                                                               Expressed sequence tags from Pneumocystis carinii Unpublished (2000)
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Smulian, A.G., Arnold, J., Weise,
J.C., Kovacs, J. and Cushion, M.
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Pneumocystis carinii f. sp. carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
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S17B9 AGS-1 Pneumocystis
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Plate: 496007 row: F col
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606 257 1717
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                            staben@pop.uky.edu.
Location/Qualifiers
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 /organism="Pneumocystis carinii f.
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/Clone_lib="496 - stressed shoot cDNA library from
Wang/Bohnert lab"
/tissue_type="seedling"
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/lab_host="E.coli XL Gold"
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BF281142.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvil
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nhiee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Other_ESTs: EST345498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G., Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat
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                                                                                /note="Vector: pT3T7Pac; Site_1: EcoR1;
Combination of ROV, RBR, RKI, RLI, RPL,
                                                                                                                                             norvegicus cDNA"
/tissue_type="mixed tissue"
/lab_host="DH5-alpha"
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//lab host="E. coli"
//note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
//note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
//note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
//note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
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                                                                                                                                                                                                                                                                              /clone="RGIAB64"
                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                       /clone_lib="Rat Gene Index, normalized rat, Rattus
                         RHE, RPC,
38 c
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/clone_lib="AGS-1"
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100.0%;
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Pred. No.
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3' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               contact the ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                   Site_2: Not1; RLU, REM, RMU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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Query Match
Best Local Similarity
Matches 62; Conserv

ilarity 100.0%; I Conservative 0;

6.0%; Score 62; DB 11; 00.0%; Pred. No. 3.7e-05;

Length 257;

Indels

0;

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Mismatches

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RESULT
AAB66939
ID AAB6
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
   e.g.
                                                                                                                   Thorens B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTX1
                                                                                                                                                    (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                          14-JUL-2000;
                                                                                                                                                                                                                                                                                                                             18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; murine; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                     WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
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                     prevention,
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                                                                             2001-112615/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
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                                                                                                                                                                                        99US-0143907.
99US-0151140.
2000US-0184285.
2000US-0616132.
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                                                                                                                                                                                                                                                                                        2000WO-IB01042
encoding GLUTX glucose transporter proteins, useful
n, diagnosis and treatment of hexose transport disor
and diabetes -
                                   encoding
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Pred. No. 3.1e-64;
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               disorders,
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DЬ QΥ Ъ QY

Claim 11;

Page 74-75;

124pp; English.

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB56932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischamia, diabetes,

Claim 11; Page 73-74; 124pp; English.

Ġ

ischemia and diabetes

Nucleic acids encoding GLUTX glucose transporter proteins, the prevention, diagnosis and treatment of hexose transport

useful in disorders

invention relates to GLUTX proteins (AAF55865-AAF5587] and 366941). The GLUTX proteins are related to the facultative

Sequence

477 AA;

neurodegenerative disease. The present sequence

hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or

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murine

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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLA-) UNIV LAUSANNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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99US-0151140.
2000US-0184285.
2000US-0616132.
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93.2%;
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ischemia and diabetes

Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders,

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  Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorder:
                                                                                                         23-FEB-2000;
13-JUL-2000;
                                                                                   (UYLA-) UNIV LAUSANNE.
                                                                                                                             14-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                   18-JAN-2001
                                                                                                                                                                                                       WO200104145-A2
                                                                                                                                                                                                                                                                                            GLUTX;
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                                                                                                                                                                                                                                                                       nypoglycaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX1.
                                                                                                                                                                                                                                                                                   hexose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363
                                                                                                                                                                                                                                                                                                                                                                                                                              prevention, diagnosis ischemia and diabetes
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                                           2001-112615/12
                                                                                                                                                                                                                                                              gene therapy; vaccine; hexose transport modulator; human; rat;
transport disorder; ischaemia; diabetes; hyperglycaemia; murine;
ycaemia; glucose metabolism disorder; neurodegenerative disease.
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2000US-0184285.
2000US-0616132.
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Pred. No. 1.3e-55;
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aim 11; Page 74-75;

124pp;

English.

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66922-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention at treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a

sent invention relates to GLUTX BEARB66941). The GLUTX proteins

proteins (AAF55865-AAF55871 and are related to the facultative

Sequence

neurodegenerative disease. The present sequence

is murine

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Best Local
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                                                                         Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders e.g. ischemia and diabetes \cdot
                                                                                                       Claim 11; Page 73-74; 124pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FLVTKEFNSIMEILRPYGAFWLTAAFCILSVLFT
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DB; AAF55867.
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92.6%;
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Pred. No. 5.
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5.6e-53;
                                                                                                                                    transport disorders,
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27 - AUG - 1999;
23 - FEB - 2000;
13 - JUL - 2000;
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                                                         hypoglycaemia; glucose metabolism
                                                                               Rat; GLUTX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280;
                                                                                                                                                                                                                                                                             Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF120840
BF120840.1 GI:10959880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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                    81405.44.19 2003
                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                   Plate: LLAM9192 row: d column: 12
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/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/clone_lib="Rat PC-12 cells, NGF-treated (5 days)"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
xhoI; poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"
a 102 c 80 g 88 t 1 others
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136437 MARC
BE231636
BE231636.1
                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized EST discovery in s_{\rm wine}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 546) Frahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa
                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 70 row: A column: 2
                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt_trimmed v0.980904.e. Vector identified by cross_match with the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
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                                                                                                                                                                                                                                                                PCR PRimers
                                                                                                                                                                                                                                                                                  and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                          /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                              Location/Qualifiers
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:9016354
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Pred. No. 2.8e-47;
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                                                        AGAGAAT - GTTCTTGTCTTGTCAACCAAGTCCTTCTCAGAGTGCCCCAGAGACCTCCGGAT
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95396786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nhlee@tigr.org
For clone availability please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (tdbinfo@tdb.tigr.org)
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
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/db_xref="ATCC (inhost):2005377"
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CCNCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGT
                                                                                                                                           CANCATGTGCCTCTTTCNATCGCCNGCTTTTGCGGTGGGCTGGGGGGCCCATCCCCTTGGC
                                                                    TCCTCATGTCAGAGATCTTCCCCCCTCGCACTNTCAAGGGCGTGGCGACAGGCATCTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prime, mRNA sequence. AL565390
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AL565390 LTI_FL013_FBrn1
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BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                           Technologies: Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Cloned into the Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week)"
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/clone_lib="LTI_FL013_FBrn1"
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/db_xref="taxon:9606"
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On Apr 26, 2001 this sequence version replaced q1:13277497.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP succession on the feature table with their source databases: Em. EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP succession on the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone RP11-356B19 The true left end of clone RP11-373J8 is at 96439 in this sequence. The tright end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
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/note="Single clone region. Sequence from reads from short insert library derived from a single pUC clone. Restriction digest data confirm the assembly." 225123. .225370
                                                                                                                                                                                                                                     /clone="RP11-356B19"
/clone_lib="RPCI-11.2"
23455. .23821
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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Location/Qualifiers
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                                Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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/protein_id="CAC51153.1"
/protein_id="CAC51153.1"
/protein_id="CAC51153.1"
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/db_xref="GI:15209698"
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VQLMVVVGILLAYLAGWYLEWRMLAVLGCVPPSLMLLMCFMPETPRFLLTQHRROEA
VQLMVVVGILLAYLAGWYLEWRMLAVLGCVPPSLMLLMCFMPETPRFLLTQHRROEA
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/db_xref="taxon:9606"
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Localization and DNA sequence of a replication origin in the rhodopsin gene locus of Chinese hamster cells J. Mol. Biol. 224 (2), 343-358 (1992)
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Direct Submission
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7929. .8097
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THQGSNFGPIFMTLPAFFAKSSSIYNPVIYIMMNKQFRNCMLTTLCCGKNILGDDEAS
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Search completed: February 13, 2002, 20:07:08 Job time: 23045 sec

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/db_xref="GI:8250661"

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                      Sequence 7 from patent US 5840568. AR060385
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Gray, J., Collins, C., Hwang, S., Godfrey, T.,
Genes from the 20013 amplicon and their us.
Patent: US 5892010-A 4 06-APR-1999;
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GEQIINIQRYKOKLEKEKSEMKMEIDDLASMEVISKSKOLEKMCRTLEBOVSELKT
KEEEDOORLINELTAORGRLOTESGEYSROLDEKDSLVSOLSRGKOAFTOOLEELKKOL
EEVKAKSALAHALOSSRHDCDLLEGY EEEQEAKAELORAMSKANSEVAOMFTKYET
DAIORTEELEBAKKKLAORLODAEEHVEAVNAKCASLEKTKORLONEVEDLMIDVERT
NAACAALDKKORNFDKILAEWKOKYEETHAELBASQKESSESSLSTELFKIKNAYEESID
OLETLKRENKHLOQEISDLTEOLAEGGKRIHELEKSIKKOLEORAELEABASL
EHEBGKILRIOLELNOVKSEIDRKIAEKDEEIDOLKRNHIRVVESNOSTLDAEIRSRN
DAIRIKKKMEGDLNEMEIQUANSTAAELARNVRNTOGILKDTOLLHDDALRGOEDL
KEOLAMVERRANLLOAEISELEAATLEOTERSRKIA HOELEK HOEDILDAEIRGRD
DAIRIKKKMEGDLNEMEIQUANSTAATORTHURVSENOSTLDAEIRGRN
TKKLETDISOIOGEMEDIVOEARNAEBEKKKAITDAAMMAEELKKEOOTSAHLERMK
KNLEOTVKDLOHIRLDEAEQLALKGGKKOIOKLEARVRELEGEVENEOKRNVEAIKGLR
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Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 518)
                                                                     Nicotiana
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1 (bases 1 to 380)
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98141129
                                                                                                                                                                                                                                                                                                                                                             Submitted (29-MAR-1997) to the DDBJ/EMBL/GenBank databases. Kiyonobu Ueno, Osaka University Medical School, Department of Medicine III; 2-2, Yamada-oka, Suita, Osaka, Japan, Suita, Osaka 565, Japan (E-mail:ueno-k@kinchu.hosp.go.jp, Tel:06-879-3835, Fax:06-879-3839)
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                                                                                                                                                                                                                                                                             Weno, K., Kumagai, T., Kijima, T., Kishimoto, T. and Hosoe, Cloning and tissue expression of cDNAs from chromosome which is frequently deleted in advanced lung cancer Hum. Genet. 102 (1), 63-68 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1228)
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/db_xref="taxon:4097"
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/clone="843Ex"
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/db_xref="taxon:9606"
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Coldren,C., Flint,D., Hallahan,D.L. and Wang,H.
Cis-prenyltransferases from plants
Patent: WO 0121650-A 1 29-MAR-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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Sequence 1 from
AX101122
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Voelker,T.A. and Davies,H.M.
Medium-chain thioesterases in plants
Patent: US 5455167-A 10 03-OCT-1995;
                                                                                                                                                                                                                   Sequence 10
I14842
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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. 7.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-355B19 The truleft end of clone RP11-373JB is at 96439 in this sequence. The right end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP11-356B19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr9
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/clone_lib="RPCI-11.2"
23455. .23821
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/db_xref="taxon:9606"
/chromosome="9"
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100.0%; Pred. No. 8e-233;
tive 0; Mismatches 0
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SOURCE
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                                                                                              STS
                                                                                                                                source
                                                                                                                                                               Prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
The Institute for Genomic Research
The Contact Center Dr., Rockville,
                                                                                                                                                                                                                                              Buffer:
                                                                                                                                                                                                                                                                                                                                     Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                              Primer A: AAGTCTTTATTTGGCAAAC
Primer B: CCTCTAGGATCTTTGTCTTC
STS size: 120
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 120)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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STS; STS sequence;
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36 c 26 g
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Location/Qualifiers
                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Triton X-100:
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KCl:
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Primer:
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          Length 120;
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Database :
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Listing first 45 summaries
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282
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## SUMMARIES

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## ALIGNMENTS

FEATURES source	MEDLINE COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 H34451 LOCUS
The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhleetigr.org For clone availability please contact the TIGR Database (tdbinfo@tdb.tigr.org) Seq primer: M13 Reverse. Location/Qualifiers 1. 319 /organism="Rattus sp." /db_xref="ATCC (inhost):2005510"	95396786 Contact: Lee, NH	A.R., Fraser C.M. and Venter J.C. Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment Proc. Natl. Acad. Sci. U.S.A. 92 8303-8307 (1995)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  1 (bases 1 to 319)  1 (bases 1 to 319)  1 (bases 1 to 319)  1 (bases 1 to 319)	end similar to Glucose transporter, mRNA sequence. H34451 H34451.1 GI:979868 EST. Rattus sp. Rattus sp.	H34451 319 bp mRNA EST 13-MAR-1998

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RESULT
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                                                                                                                                                                                                                                                              Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre-
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9192 row: d column: 12
Plate: LLAM9192 row: d column: 12
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600 67:48:40 Fr
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
xho1: poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"
a 102 c 80 g 88 t 1 others
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Pred. No. 5.2e-61;
""" matches 2;
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Sus scrofa
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136437 MARC
BE231636
                                                                                                                                                                                                                                USDA, ARS, US Meat Animal PO Box 166, Clay Center, I Tel: 402 762 4366 Fax: 402 762 4390
                                                                                         BACKWARD: GTTTTCCCAGTCACGACG
Plate: 70 row: A column: 21
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                        Fahrenkrug, S.C., Stone, R.T., Heat
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                                                                                                                                                                                                                                                                                               Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                                                                                                            and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
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                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
/clone_lib="MARC lPIG"
/tissue_type="pooled"
                                /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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90.9%;
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tcaccttggggttagccagcttacccatcacttacaggttctctcccaactctcagctggt
                                                                                                                                          agggacttagccacataagatttgggctcagaaacaaggtcaggtgagtccaggaagaaa 786
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                                                       AGAGAAT-GTTCTTGTCTAACCAAGTCCTTCTCAGAGTGCCCCAGAGACCTCCGGAT
                                                                        agagaatggttcttgtcttgtcaaccaagtccttctcagagtg-ccaaagacctccggat
                                                                                                                        AGGGACTTAGCCACATAAGATTTGGGCTCAGAAACAAGGTCAGGTGAGTCCAGGAAGAAA
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                                                                                                                                                                                                                                                                   298;
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EST111272 Rat PC-12 of
clone RPNBT28 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earl, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lee, NH
The Institute for Genomic R
9712, Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (tdbinfo@tdb.tigr.org)
Seq primer: Ml3 - 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone availability please
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                        98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript SK-, Site_1: EcoRi; Site_2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT prin
                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus sp."
/db_xref="ATCC (inhost):2005377"
/db_xref="taxon:10118"
/clone="RPNBT28"
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                                                                                                                                                                                                                                                                                                                                                                 directionally cloned using the Lambda ZAP II Vector by Stratagene" 78 t 4 others
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95.5%;
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cells, N
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                                                                                                                                                                                                                                                              Score 229; DB 11;
Pred. No. 4.7e-22;
0; Mismatches 8;
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.D., Adams,M.D., Kerlavage
                                                                                                                                                                                                                                                                                                Length 324;
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TITLE
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Best Local :
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                CTCAGTGTCCTGGATCATTAGTCACCAGGTCTTGTGAGTTTCAG-AAAATNAAAGGCCT
CCNCACCAACTGGCTCATGGCCTTTCTCGTGACCAAGGAGTTCAGCAGCCTCATGGAGGT 492
                                                                                                                              CANCATGTGCCTCTTTCNATCGCCNGCTTTTGCGGTGGGCTCGGGGGGCCCATCCCCTTGGC 612
                                                                                                                                                                                             SGCGCCTGTCTCTGCACAGCCTGTTGATGCCAGCGTGGGCCTSGCCTGGCTGGCCGTGGN 672
                                                                                  tcctcatgtcagagatctt--ccctctgcacatcaagggtgtgggctaccggcgtctgtgt 230
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                                                                TCCTCATGTCAGAGATCTTCCCCCTCGCACTNTCAAGGGCGTGGCGACAGGCATCTGCGT 552
                                                                                                                                                                                                                                                                290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li,W.B., Gruber,C., Jessee,J. a Full-length cDNA libraries and Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL565390 752 bp mRNA EST 16-FEB-2001
AL565390 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSODF005YE02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National BP 191 91006 EVRY cedex - F:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                         end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CSODF005YE02"
/clone_lib="LTI_F1013FBrn1"
/dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: Fetal brain; Vector: pCMVSPORT 6; 1st cDNA was primed with a NotI-oligo(dT) primer. Five \mathfrak p
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79.5%;
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Primates;
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                                                                                                                                                                                                                                                                            Score 218.6; DB 1
Pred. No. 8.4e-21;
                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all reg&ns were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: Sw:, Continuous and the continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous co
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Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 225370)
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During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mappi Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
on Apr 26, 2001 this sequence version replaced gl:13277497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPI1-356B19 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RP11-356B19 The true left end of clone RP11-373J8 is at 96439 in this sequence. The tright end of clone RP13-225021 is at 9980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
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   /note="Single clone region. Sequence from reads short insert library derived from a single pUC c Restriction digest data confirm the assembly." 225123. .225370
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/db_xref="taxon:9606"
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Pred. No. 9.1e-12;
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Patent: WO 0149728-A 29 12-JUL-2001
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                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                               Similarity 100.
23; Conservative
(bases 1 to 11931)
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VQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
61. .849
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7e-12;
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Localization and DNA sequence of a replication origin in the rhodopsin gene locus of Chinese hamster cells
J. Mol. Biol. 224 (2), 343-358 (1992)
92219256
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10702...10812)
/gene="Thopdopsin"
6107...10812
/gene="Thodopsin"
join(6107...6467,7929...8)
10702...10812
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IFFCYGOLVFTVKEAAAQQQESATTQKAEKEVTRMVILMVVFFLICWFPYAGVAFYIF
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/translation="MKGTEGPHYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYM
fLLLVLGFPINFLTLYVYQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGY
FVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVLCKPMSNFFGEBHHAIMGVVFT
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/protein_id="CAA43398.1"
/db_xref="GI:49479"
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/cell_line="CHO"
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/db_xref="taxon:10029"
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7929. .8097
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/rpt_family="Alu"
10702. .>10812
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/gene="rhodopsin"
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/gene="rhopdopsin"
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                                                                                                   /number=4
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BASE COUNT
ORIGIN
                                             repeat_region
                /number=5

jion 11409. 11462

/note="triplex motif (GA)"

2719 a 3172 c 3122 g 2918 t
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Ouery Match 7.4%; Sc
Best Local Similarity 100.0%; F
21;
             Score 21; DB 10; Length 11931; Pred. No. 1.2;
   red. No. 1.2;
Mismatches'
    0; Indels
    0;
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Gaps

0

Search completed: February 13, 2002, 20:07:08 Job time: 23045 sec

Вþ Qγ

/product="myosin heavy chain" /protein_id="AAB29713.2"

FEX

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DEFINITION ACCESSION
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AR070327
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AR060385
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                               AR060385 2085 bp DN
Sequence 7 from patent US
AR060385
                                                                                                                                                                                                                                                                                                                                                                                                               Gray,J., Collins,C., Hwang,S., Godfrey,T., Kowbel,D. and Rommens,J Genes from the 20013 amplicon and their uses
Patent: US 5892010-A 4 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AR070327 2605 bp
Sequence 4 from patent
AR070327
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1. .2605
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/db_xref="GI:8250661"
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Pred. No.
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Pred. No.
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US 5840568
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5.4e-22;
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Best Local Similarity 100
Matches 57; Conservative
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                                                   Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 518)
                                                           Nicotiana tabacum (strain:bright yellow 2) cDNA to
                                                                                                        Nicotiana
AB005878
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AX062918
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                                                                                           AB005878.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0100828-A 545 04-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
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Hodgkin's disease associated molecules and uses thereof Patent: US 5840568-A 7 24-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 380)
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                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .380
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545 from Patent WOO100828
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1 76 c 102 g
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398 c 557 g
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100.0%; Pr
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100.0%; Pred. No.
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mRNA
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Pred. No.
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8.4e-21;
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56; Conser
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                                                                                                                                                                                                                                                                         Cloning and tissue expression of cDNAs from chromos which is frequently deleted in advanced lung cancer Hum. Genet. 102 (1), 63-68 (1998)
                                                                                                                                                                                                                                                                                                                                                         Kiyonobu Ueno, Osaka University Medical School, Department of Medicine III; 2-2, Yamada-oka, Suita, Osaka, Japan, Suita, Os 565, Japan (E-mail:ueno-k@kinchu.hosp.go.jp, Tel:06-879-3835, Fax:06-879-3839)
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/protein_id="BAA21615.1"
/db_xref="GI:2280518"
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56; Conserva
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/db_xref="taxon:13490"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone concigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9______
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/note-"Single clone region. Sequence from reads from short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-356B19"
/clone_lib="RPCI-11.2"
23455. .23821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.5%; Score 463; DB 9;
100.0%; Pred. No. 8e-233;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 225370;
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ACCESSION
VERSION
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ORGANISM
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G20347/c
LOCUS
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                                                                                              Matches
                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
         1758 ttgtttgccaaataaagac 1776
                                      source
   21
TTGTTTGCCAAATAAAGAC
                                                                                              79;
                                                                                                        Similarity
                                                                                                                                                                                                                                                         Prepared with primer pairs derived Numbers - R17700, T59518, T59564
                                                                                                                                                                                                                                                                                                                                                            Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: AAGTCTTTATTTGGCAAAC
Primer B: CCTCTAGGATCTTTGTCTTC
STS size: 120
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G20347
G20347.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS; STS sequence; primer; sequence tagged site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G20347
                                                                                            Conservative
                                                                                                                                                                   39
                                                                                                                                                             complement(101. .120)
. 36 c 26 g
                                                                                                                                                                                                                                                                                            Tris-HCl pH8.8: 100 rKcl: 500 mgCl2: 20 m Triton X-100: 1% Concentration: 10X
                                                                                                                                                                                                                                                                                                                                                                             GenomicDNA: 25 ng
Primer: 0.43 uM each
dNTPs: 230 uM each
AmpliTaq: 0.5 units
TaqStart Ab: 0.5 units
Total Volume: 10 u1
                                                                                                                                                                                          1. .19
                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 bp DNA
A005N15, sequence tagged site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denaturation:
                                                                                                      4.48;
                                                                                        score 79; DB Pred. No. 6e-0; Mismatches
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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72C
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30sec
5min
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30sec
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                                                                                                   DB 11;
6e-30;
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                                                                                         0,
                                                                                                              Length 120,
                                                                                        Indels
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RESULT
AAB66939
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Best Local
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                                                                                                                                                                                    14-JUL-1999;
27-AUG-1999;
23-FEB-2000;
          Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                     GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; murine; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                    Thorens B,
                                                                                                                                                                                                                                                          14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUTX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66939 standard; Protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX1.
                                                                                                                                    (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                             18-JAN-2001
                                                                                                                                                                                                                                                                                                                           WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 71-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention, di . ischemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                   2001-112615/12.
                                                                                                                                                                                                                                                                                                                                                             sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478
                                                                                                    Ibberson M,
                                                                                                                                                                    99US-0143907.
99US-0151140.
2000US-0184285.
2000US-0616132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                        2000WO-IB01042
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diagnosis and treatment of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.5%;
100.0%;
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                                                                                                  uldry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 478;
            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474
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Claim 11;

Page 74-75; 124pp; English.

AAB66932-AAB66941).

invention re

relates to GLUTX proteins (AAF55865-AAF5587] and he GLUTX proteins are related to the facultative

Sequence

The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66332-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport

function. The GLUTX proteins may be used in the diagnosis, preventic treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or neurodegenerative disease. The present sequence is murine GLUTX1.

prevention

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AAB66934
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Best Local
                                                                                               Claim 11; Page 73-74; 124pp;
                                                                                                                    e.g. ischemia and diabetes
                                                                                                                          Nucleic acids encoding GLUTX glucose transporter proteins, the prevention, diagnosis and treatment of hexose transport
                                                                                                                                                            N-PSDB;
                                                                                                                                                                                         Thorens B,
                                                                                                                                                                                                                                13-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                          Murine; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention at treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence
                                                                                                                                                                                                            (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                           23-FEB-2000;
                                                                                                                                                                                                                                                    27-AUG-1999;
                                                                                                                                                                                                                                                              14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                        Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
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                                                                                                                                                                    2001-112615/12.
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                                                                                                                                                                                                                                                                                                                                                                                                        GLUTX1
                                                                                                                                                            AAF55867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 93.2
10; Conservative
                                                                                                                                                                                        Ibberson
                                                                                                                                                                                                                                2000US-0184285
2000US-0616132
                                                                                                                                                                                                                                                                                  2000WO-IB01042
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                                                                                                                                                                                                                                                   99US-0143907
99US-0151140
                                                                                                                                                                                        X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%;
93.2%;
                                                                                                                                                                                                                                                                                                                                                             metabolism disorder; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                477
                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 598; DB 22;
Pred. No. 7.2e-61;
5; Mismatches 3
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                                                                                                                                    useful in
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RESULT
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the prevention, diagnosis and e.g. ischemia and diabetes -
          Nucleic acids encoding GLUTX glucose transporter proteins, useful the prevention, diagnosis and treatment of hexose transport disord
                                                                                                                                                                14-JUL-1999;
27-AUG-1999;
                                                        WPI;
                                                                                  Thorens
                                                                                                                                                                                                         14-JUL-2000; 2000WO-IB01042
                                                                                                                                                                                                                                      18-JAN-2001
                                                                                                                                                                                                                                                                                                                                           GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; murine; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66942). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is rat GLUTX1.
                                                                                                            (UYLA-) UNIV LAUSANNE
                                                                                                                                       13-JUL-2000;
                                                                                                                                                                                                                                                                  WO200104145-A2
                                                                                                                                                                                                                                                                                                                                                                                                        GLUTX1 consensus
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                                                                                                                                                    23-FEB-2000;
                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB66939 standard; Protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWFMA 60
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                                                                                                                                                                                                                                                                                            qs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
                                                                                Ibberson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                       2000US-0184285
2000US-0616132
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                99US-0143907
99US-0151140
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                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                               Uldry
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Pred. No. 1.3e-55;
Mismatches 0;
                                                                                Z
          transport disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 478;
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                        in
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Claim 11; Page 74-75; 124pp; English.

resent invention

AAB66941).

The GLUTX

proteins

proteins (AAF55865-AAF55871 and are related to the facultative

hyperglycaemia, hypoglycaemia, neurodegenerative disease. The

477

function. The GLUTX proteins may be used in the diagnosis, prevention treatment of hexose transport disorders such as ischaemia, diabetes,

and

nia, a glucose metabolism disorder and/or The present sequence is murine GLUTX1.

relates to GLUTX

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RESULT
AAB66934
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Matches
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27-AUG-1999;
23-FEB-2000;
13-JUL-2000;
                                                                The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
                                                                                                                  Claim 11; Page 73-74;
                                                                                                                                          Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention at treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence for GLUTX1.
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